

DR N-PSDB; AAV65294.
 XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
 PT for evaluating gene expression, and identification of virulence
 PT genes

XX Claim 3; Page 177; 333pp; English.

XX This sequence represents a Streptococcus pneumoniae protein of unknown
 CC function. The invention provides DNA sequences (AAV65201 to AAV65304)
 CC from the Streptococcus pneumoniae genome and corresponding protein
 CC sequences (AAV650605 to AAV650728). The protein sequences are classified as
 CC hypothetical, cell wall biosynthetic, external target, or minimal gene
 CC set proteins. A recombinant host containing a vector comprising any of
 CC the above nucleic acids can be used for the recombinant expression of the
 CC proteins. The invention also provides a DNA chip having arrayed on it at
 CC least 15 base pair fragment of any one or more of these DNA sequences.
 CC The DNA chip can be used methods for evaluating gene expression in S.
 CC pneumoniae and for identifying virulence genes in S. pneumoniae.
 CC Antibodies that selectively bind to the above proteins or peptide
 CC fragments can be used to treat S. pneumoniae infection. The antibodies
 CC can also be used to detect S. pneumoniae cells.

XX Sequence 122 AA;

Query Match 100.0%; Score 618; DB 19; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2,7e-69;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMIVGHGIDIEELASISAVTRHGGFAKRVLTQEMERFTSLKGRQIEYLAGRWSAKE 60
 Db 1 MRMIVGHGIDIEELASISAVTRHGGFAKRVLTQEMERFTSLKGRQIEYLAGRWSAKE 60

QY 61 AFSKAMGTGTSKLGFDLEVLNNGGAPYFSQAPFSCKIWLISHTDQFVTASVILEBNH 120
 Db 61 AFSKAMGTGTSKLGFDLEVLNNGGAPYFSQAPFSCKIWLISHTDQFVTASVILEBNH 120

QY 121 ES 122
 121 ES 122
 121 ES 122

RESULT 2
 AAU37879
 ID AAU37879 standard; Protein; 122 AA.

XX AAU37879;
 XX
 DT 14-FEB-2002 (first entry)

DE Streptococcus pneumoniae cellular proliferation protein #308.

KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.

OS Streptococcus pneumoniae.

XX MO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

XX 23-MAY-2000; 2000US-206848P.

XX 26-MAY-2000; 2000US-207272P.

XX 23-OCT-2000; 2000US-242578P.

XX 27-NOV-2000; 2000US-253625P.

XX 22-DEC-2000; 2000US-257931P.

XX 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

XX

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 DR WPI; 2001-611495/70.
 DR N-PSDB; AAS55738.

PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX Example 3; Seq ID No 13472; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 122 AA;

Query Match 100.0%; Score 618; DB 22; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2,7e-69;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMIVGHGIDIEELASISAVTRHGGFAKRVLTQEMERFTSLKGRQIEYLAGRWSAKE 60
 Db 1 MRMIVGHGIDIEELASISAVTRHGGFAKRVLTQEMERFTSLKGRQIEYLAGRWSAKE 60

QY 61 AFSKAMGTGTSKLGFDLEVLNNGGAPYFSQAPFSCKIWLISHTDQFVTASVILEBNH 120
 Db 61 AFSKAMGTGTSKLGFDLEVLNNGGAPYFSQAPFSCKIWLISHTDQFVTASVILEBNH 120

QY 121 ES 122
 121 ES 122
 121 ES 122

RESULT 3
 AAU38056
 ID AAU38056 standard; Protein; 122 AA.

XX AAU38056;

XX 14-FEB-2002 (first entry)

DE Streptococcus pneumoniae cellular proliferation protein #485.

KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.

OS Streptococcus pneumoniae.

XX MO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

XX 23-MAY-2000; 2000US-206848P.

XX

XX

XX

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PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-255625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Hasselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PSDB; AAS55915.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 13649; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
SQ Sequence 122 AA;
XX
Query Match: 100.0%; Score 618; DB 22; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.7e-63;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY 1 MRMIYGHIDIEELASIESAVTRHGGPAKRVLTAAQEMERFTSLKRRQIEYLAGRWSAKE 60
Db 1 MRMIYGHIDIEELASIESAVTRHGGPAKRVLTAAQEMERFTSLKRRQIEYLAGRWSAKE 60
QY 61 AFSKAMGTGISKLGFDIEVLNNRGAAPYFSQAPPSGKTIWLSISHTDQVTVASVILEBNH 120
Db 61 AFSKAMGTGISKLGFDIEVLNNRGAAPYFSQAPPSGKTIWLSISHTDQVTVASVILEBNH 120
QY 121 ES 122
Db 121 ES 122
XX
RESULT 4
ID AAY88388
ID AAY88388 standard; Protein; 156 AA.
XX
AC AAY88388;
XX
DT 25-JUL-2000 (first entry)
XX
DE S-ydCB essential bacterial protein amino acid sequence.
XX
KM Bacteria; S-ydCB, Streptococcus pneumoniae; antibacterial compound;
XX acyl carrier protein synthase; identity; bacterial infection; treatment.
XX
OS Streptococcus pneumoniae.
XX

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XX XN WO200018952-A1.
XX PD 06-APR-2000.
XX PF 30-SEP-1999; 99WO-US22666.
XX PR 30-SEP-1998; 98US-0163446.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Filtz C, Youngman P, Guzman L;
XX DR WPI; 2000-303457/26.
XX DR N-PSDB; AAA13270.
XX PT Identifying new antibacterial agents particularly against Streptococcus
XX PF pneumoniae, uses S-ydcb polypeptide from S. pneumoniae and B-ydcb
XX PT polypeptide from Bacillus subtilis -
XX XX
XX Claim 17; Fig 1; 58pp; English.
XX XX
CC This sequence represents the protein encoded by the essential bacterial
CC gene S-ydcb from Streptococcus pneumoniae. B-ydcb is an S-ydcb ortholog
CC from Bacillus subtilis. The gene encodes a protein which has structural
CC characteristics of acyl carrier protein synthase and displays synthase
CC activity in vitro. The protein is used in a method for identifying an
CC antibacterial agent, which comprises contacting an S-ydcb or B-ydcb
CC polypeptide with a test compound and detecting an interaction between the
CC polypeptide and the test compound, where the interaction indicates that
CC the compound is an antibacterial compound. Antibacterial agents
CC identified using the method may be used to treat a bacterial infection,
CC especially Streptococcus pneumoniae in mammals, especially a human or
CC rodent. The method can be configured for high throughput screening of
CC numerous candidate antibacterial agents, and identified agents should
CC have a broad spectrum of antibacterial activity.
XX SQ
XX Sequence 156 AA;
XX
XX Query Match 100.0%; Score 618; DB 21; Length 156;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-69;
XX Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY 1 MRMIVGHGIDIEELASISAVTRHGGFAKRVLTQDEMRFSLKRRQIEYLGRWSAKE 60
DB 35 MRMIVGHGIDIEELASISAVTRHGGFAKRVLTQDEMRFSLKRRQIEYLGRWSAKE 94
QY 61 AFSKAMGIGISKLGQDLELVNNGRGAFFSOAPSPGKIMTISHTDQFVTASVILENH 120
DB 95 AFSKAMGIGISKLGQDLELVNNGRGAFFSOAPSPGKIMTISHTDQFVTASVILENH 154
QY 121 ES 122
DB 155 ES 156
XX
XX RESULT 5
XX ID AAYS8607 standard; Protein; 120 AA.
XX AC AAYS8607;
XX DT 11-APR-2000 (first entry)
XX DE Streptococcus pneumoniae acyl carrier protein synthase acps.
XX KM Acyl carrier protein synthase; acps; infection; therapy;
XX KM diagnosis; antibacterial; antibiotic; Helicobacter pylori.
XX OS Streptococcus pneumoniae.
XX XX
XX WO9961452-A2.
XX PD 02-DEC-1999.

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XX 27-MAY-1999; 99WO-US11704.
PF
XX 28-MAY-1998; 98US-0087079.
PR
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA
XX Pearson SC, Kallender H;
PI
XX WPI; 2000-147027/13.
DR N-PSDB; AAZ5350.
XX
XX New isolated Streptococcus pneumoniae acps polypeptides, used to
PT develop products for treating, e.g. otitis media -
XX
XX Claim 1; Page 31-32; 34pp; English.
PS
XX
CC The present sequence represents the acps protein of
CC Streptococcus pneumoniae strain 010093 (NCIMB 40794), which is
CC phylogenetically related to proteins of the acyl carrier protein
CC synthase family. The invention provides acps polypeptides having
CC having at least 70% identity with the present sequence, as well as
CC acps polynucleotides, recombinant materials and methods for their
CC production. The polypeptides or treatment of a disease related to the
CC the diagnosis, prognosis or treatment of a disease related to the
CC expression or activity of acps. They can be used to treat microbial
CC diseases such as bacterial infections, particularly S. pneumoniae
CC infections, to prevent infections and to identify agonists and
CC antagonists useful as antibacterial compounds. They can also be
CC used to prevent bacterial adhesion to mammalian, extracellular
CC matrix proteins on in-dwelling devices or to extracellular matrix
CC proteins in wounds, to block bacterial adhesion between mammalian,
CC extracellular matrix proteins and bacterial acps proteins that
CC mediate tissue damage and/or to block the normal progression of
CC pathogenesis in infections other than by the implantation of
CC in-dwelling devices or by other surgical techniques. The
CC antibacterial compounds can be used in the treatment of
CC Helicobacter pylori (Hp) infections, to decrease the advent of
CC Hp-induced cancers, such as gastrointestinal carcinoma, and also to
CC prevent, inhibit and/or cure gastric ulcers and gastritis. They
CC can also be used for treating e.g. otitis media, conjunctivitis,
CC pneumonia, bacteraemia, meningitis, sinusitis, pleural empyema and
CC endocarditis.
CC
XX Sequence 120 AA;
SQ
Query Match 98.4%; Score 608; DB 21; Length 120;
Best Local Similarity 100.0%; Pred. No. 4,7e-68;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERFTSLKGRQTEYLGRWSAKEAF 62
DB 1 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERFTSLKGRQTEYLGRWSAKEAF 60
QY 63 SKAMGTGISKLGQDLEVLNNEGAPYFSQAPFSGKIWLSISHTDQCVTASVILEENHES 122
DB 61 SKAMGTGISKLGQDLEVLNNEGAPYFSQAPFSGKIWLSISHTDQCVTASVILEENHES 120

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06 Streptococcus pneumoniae type 4 strain.
XX
XX WO200277021-A2.
PN
XX 03-OCT-2002.
XX
XX 27-MAR-2002; 2002WO-IB02163.
XX
XX 27-MAR-2001; 2001GB-0007658.
PR
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
XX Masignani V, Tettelin H, Fraser C;
PI
XX WPI; 2003-040579/03.
DR N-PSDB; ABX07464.
XX
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection -
XX
XX Claim 1; SEQ ID No 3504; 56pp; English.
PS
XX
CC The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC AB556454. Also included are an antibody which binds one of the
CC proteins, treating a patient by administering the protein, DNA or
CC antibody (in a composition), a kit comprising first and second primers,
CC which are the nucleic acid cited above or fragments between nucleotides
CC 8-100 of a sequence not defined in the specification, for amplifying a
CC target sequence contained within a Streptococcus nucleic acid sequence,
CC where the first primer is substantially complementary to the target
CC sequence and the second primer is substantially complementary to the
CC complement of the target sequence, and where the parts of the primers
CC having substantial complementarity define the termini of the target
CC sequence to be amplified, assay comprising contacting a test compound
CC with the protein, and determining whether the test compound binds to the
CC protein and a Streptococcus pneumoniae bacterium, where one or more
CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is one of
CC the 2469 proteins expressed by the identified coding regions from the
CC genomic sequence.
CC
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX Sequence 120 AA;
SQ
Query Match 98.4%; Score 608; DB 24; Length 120;
Best Local Similarity 100.0%; Pred. No. 4,7e-68;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERFTSLKGRQTEYLGRWSAKEAF 62
DB 1 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERFTSLKGRQTEYLGRWSAKEAF 60
QY 63 SKAMGTGISKLGQDLEVLNNEGAPYFSQAPFSGKIWLSISHTDQCVTASVILEENHES 122
DB 61 SKAMGTGISKLGQDLEVLNNEGAPYFSQAPFSGKIWLSISHTDQCVTASVILEENHES 120

```

RESULT 7

KM group A streptococcus; Streptococcus pyogenes; antibacterial;
KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
OS Streptococcus agalactiae.
XX
XX MO200234771-A2.
PN
XX
PD 02-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-GB04789.
PE
XX
XX 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-MAR-2001; 2001GB-0005640.
XX
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tetteijn H;
XX
DR WPI: 2002-352536/38.
DR N-PSDB; ABN67856.
XX
PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX
XX Claim 1; Page 3516; 4525pp; English.
PS
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX
XX Sequence 119 AA;
SQ
Query Match 53.2%; Score 328.5; DB 23; Length 119;
Best Local Similarity 52.1%; Pred. No. 5.3e-33;
Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
QY 3 MIVGHGDIIEFLASIESAVTRHEGFAKRVLTAEOMERTSLKG-RROEYLAGRMSAKEA 61
DB 1 MIVGHGIDLEIETITKAYERNORPAERVLTEQELIKXG(SNPRQMSF)TGRWAKEA 60
QY 62 FSKAMGTGISKLGFOLEVLNNERGAPYFSQAPFSKGIMWISHTDQFVTASVILEE 118
DB 61 YSKALGTGICGVNHHIDILSDDKGAPLITKEPFNGKSFVSISSGNVAQSVILLE 117
RESULT 10
ABBS4157
ID ABBS4157 standard; Protein; 119 AA.
XX
AC ABBS4157;
XX
XX 16-MAY-2002 (first entry)
XX
XX Lactococcus lactis protein acps.
XX

KM Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX
XX Lactococcus lactis IL1403.
OS
XX
XX FR2807446-A1.
PN
XX
PD 12-OCT-2001.
XX
XX 11-APR-2000; 2000FR-0004630.
XX
XX 11-APR-2000; 2000FR-0004630.
PR
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA
PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX
XX WPI: 2002-043418/06.
DR
XX
XX New nucleotide sequence useful in the identification or Lactococcus
PT lactis and related species -
XX
XX Claim 6; SEQ ID No 859; 2504pp; French.
PS
XX
XX The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABAS90521) and related proteins (ABBS3300-ABBS5621). The
CC nucleic acid sequence is useful in the detection and/or amplification of
CC nucleic acid sequence, particularly to identify Lactococcus lactis or
CC related species. The proteins of the invention are useful for the
CC biosynthesis or biodegradation of a composition of interest. The
CC invention helps research in lactic bacteria, particularly useful in the
CC production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
CC WO200177334 (published 18-OCT-2001) which is available in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 119 AA;
SQ
Query Match 48.9%; Score 302; DB 23; Length 119;
Best Local Similarity 51.3%; Pred. No. 1.1e-29;
Matches 61; Conservative 25; Mismatches 31; Indels 2; Gaps 2;
QY 3 MIVGHGDIIEFLASIESAVTRHEGFAKRVLTAEOMERTSLKG-RROEYLAGRMSAKEA 61
DB 1 MVFETGVNDELSTIQALTRSEFEVQLTAELEKXNSFOSTARKTEFLAGRWAKEA 60
QY 62 FSKAMGTGISK-LGFOLEVLNNERGAPYFSQAPFSKGIMWISHTDQFVTASVILEE 119
DB 61 FSKAYGTGFGKALGMHLEIKNDELKPKFTTKHPFDQGVHLSHSNLEAVAFVLEKN 119
RESULT 11
AAU35183
ID AAU35183 standard; Protein; 117 AA.
XX
XX AAU35183;
XX
XX 13-FEB-2002 (first entry)
XX
XX Enterococcus faecalis cellular proliferation protein #470.
DB
XX
XX Antisense; prokaryotic cellular proliferation protein;
KM antibiotic; antibacterial; drug design.
XX
XX Enterococcus faecalis.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR

26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.

(ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT,
 PI Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.
 DR N-PSDB; AAS53042.

PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -

PS Example 3; Seq ID No 10776; 511bp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 117 AA;

Query Match 48.7%; Score 301; DB 22; Length 117;
 Best Local Similarity 51.3%; Pred. No. 1.5e-29;
 Matches 59; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHGGPAKRVLTQEMERFTSLGRRQIEYLAGRWSAKEAF 62
 DB 1 MIVGHGIDIEELASIESAVTRHGGPAKRVLTQEMERFTSLGRRQIEYLAGRWSAKEAF 60
 QY 63 SKAMGTGISKLGFDQDEVLTNNRGAPYFSQAPPSGKIWISHTDQFVTASVILE 117
 DB 61 SKAMGTGISKLGFDQDEVLTNNRGAPYFSQAPPSGKIWISHTDQFVTASVILE 115

RESULT 12

AA58389
 ID AAY8389 standard; Protein; 121 AA.

AC AAY8389;

DT 25-JUL-2000 (first entry)

DE B-ydcB essential bacterial protein amino acid sequence.

KW Bacterial gene; B-ydcB; *Streptococcus pneumoniae*; antibacterial compound;
 KW acyl carrier protein synthase; identify; bacterial infection; treatment.

OS *Bacillus subtilis*.

PN WO200018952-A1.

PD 06-APR-2000.

PF 30-SEP-1999; 99WO-US22666.

XX 30-SEP-1998; 98US-0163446.

XX (MILL-) MILLENNIUM PHARM INC.

PI Fritz C, Youngman P, Guzman L;

DR WPI; 2000-303457/26.

DR N-PSDB; AAA13271.

PT Identifying new antibacterial agents particularly against *Streptococcus*
 PT *pneumoniae*, uses S-ydcB polypeptide from *S. pneumoniae* and B-ydcB
 PT polypeptide from *Bacillus subtilis* -

PS Claim 17; Fig 2; 58bp; English.

CC This sequence represents the essential bacterial protein B-ydcB from
 CC *Bacillus subtilis*. B-ydcB is an ortholog of the S-ydcB from *Streptococcus*
 CC *pneumoniae*. The gene encodes a protein which has structural
 CC characteristics of acyl carrier protein synthase and displays synthase
 CC activity in vitro. The protein is used in a method for identifying an
 CC antibacterial agent, which comprises contacting an S-ydcB or B-ydcB
 CC polypeptide with a test compound and detecting an interaction between the
 CC compound and the test compound, where the interaction indicates that
 CC the compound is an antibacterial compound. Antibacterial agents
 CC identified using the method may be used to treat a bacterial infection,
 CC especially *Streptococcus pneumoniae* in mammals, especially a human or
 CC rodent. The method can be configured for high throughput screening of
 CC numerous candidate antibacterial agents, and identified agents should
 CC have a broad spectrum of antibacterial activity.

SQ Sequence 121 AA;

Query Match 40.6%; Score 251; DB 21; Length 121;
 Best Local Similarity 44.6%; Pred. No. 2.9e-23;
 Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;

QY 3 MIVGHGIDIEELASIESAVTRHGGPAKRVLTQEMERFTSLGRRQIEYLAGRWSAKEAF 62
 DB 1 MIVGHGIDIEELASIESAVTRHGGPAKRVLTQEMERFTSLGRRQIEYLAGRWSAKEAF 60
 QY 63 SKAMGTGISKLGFDQDEVLTNNRGAPYFSQAPPSGKIWISHTDQFVTASVIL 116
 DB 61 SKAMGTGISKLGFDQDEVLTNNRGAPYFSQAPPSGKIWISHTDQFVTASVIL 116

QY 117 E 117
 DB 117 E 117

RESULT 13

AA52130
 ID AAM52130 standard; Protein; 121 AA.

AC AAM52130;

DT 01-FEB-2002 (first entry)

DE *Bacillus subtilis* ACPS.

KW *Bacillus subtilis*; ACPS; acyl carrier protein synthase; active site;
 KW protein coordinate data; CoA binding site; X-ray crystallography;
 KW Swiss Protein P96618.

OS *Bacillus subtilis*.

PN WO2000155340-A2.

PD 02-AUG-2001.

PF 26-JAN-2001; 2001WO-US02732.

PR 28-JAN-2000; 2000US-178639P.
XX
PS (AMHP) AMERICAN HOME PROD CORP.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Parris KD, Somers WS, Tam AS, Lin LL, Stahl ML;
XX
DR WPI; 2001-476201/51.
XX
PT Novel crystallized acyl carrier protein synthase enzyme used to
PT identify an activator or inhibitor of a molecule or complex comprising
PT a CoA binding site, and to determine the molecular structure of a
PT molecule or complex -
PS Disclosure; Fig 8; 181pp; English.
XX
CC The invention relates to a crystallized acyl carrier protein synthase
CC (ACPS) enzyme used to identify an agent that interacts with the active
CC site, to identify an activator or inhibitor of a molecule or molecular
CC complex comprising a CoA binding site and to determine the molecular
CC structure. The present sequence is that of the Bacillus subtilis ACPS.
XX
SQ Sequence 121 AA;
Query Match 40.6%; Score 251; DB 22; Length 121;
Best Local Similarity 44.6%; Pred. No. 2,9e-23;
Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;
QY 3 MIVGHGIDIEELASISAVTRHSGFAKRVLTAEEMERFTSLKGRQIEYLAGMSAKEAF 62
DB 1 MIVGIGDITELKRIASMAGRQKRFARILITRSLDQYELSEKRNKEFLAGRFAAKEAF 60
QY 63 SKAMGTGISK-LGFQDLEVLNNEKAPY-----FSQAPFSGKWLISHTDQVTVASVIL 116
DB 61 SKAFGTGIGRLSFQDIEIRKQNGKRYIICTKLSQA---AVHVSITHTKEYAAQAQVVI 116
QY 117 E 117
DB 117 E 117
RESULT 14
AAU10694
ID AAU10694 standard; protein; 120 AA.
XX
AC AAU10694;
XX
DT 25-FEB-2002 (first entry)
XX
DE B. subtilis ACPS used to grow ACP/ACPS complex crystals.
XX
KM Crystal structure; acyl carrier protein synthase; acyl carrier protein;
KM rational drug design method; antibiotic; 4'-phosphopantetheinyl; P-pant;
XX ACP/ACPS complex; protein co-ordinate data.
OS Bacillus subtilis.
XX
PN WO200185743-A2.
XX
PD 15-NOV-2001.
XX
PF 26-JAN-2001; 2001WO-US02949.
XX
PR 08-MAY-2000; 2000US-202466P.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Parris KD, Somers WS, Tam AS, Lin LL, Stahl ML, Powers R, Xu G;
XX WPI; 2002-055580/07.
XX
PT Crystallised complex useful in rational drug design methods, comprises

PT acyl carrier protein synthase and acyl carrier protein -
XX
XX Example 1; Fig 1; 147pp; English.
XX
CC The present invention relates to a crystallised structure comprising
CC acyl carrier protein synthase (ACPS) complexed with acyl carrier
CC protein (ACP). The invention also describes the solution structure
CC of Bacillus subtilis ACP. Both these structures are useful in rational
CC drug design methods for identifying agents that may interact with
CC active sites of ACPS and ACP, and for testing these agents to identify
CC agents that may represent novel antibiotics. They are also useful for
CC design and selection of potent and selective agents which interact with
CC ACPS and ACP, and for the design of antibiotics and other agents that
CC interfere with 4'-phosphopantetheinyl (P-pant) attachment, thus
CC preventing activation of corresponding carrier proteins. The present
CC sequence represents B. subtilis ACPS used to grow ACP/ACPS complex
CC crystals.
XX
SQ Sequence 120 AA;
Query Match 39.3%; Score 243; DB 23; Length 120;
Best Local Similarity 44.1%; Pred. No. 2,8e-22;
Matches 52; Conservative 25; Mismatches 31; Indels 10; Gaps 3;
QY 6 GHGIDIEELASISAVTRHSGFAKRVLTAEEMERFTSLKGRQIEYLAGMSAKEAFSA 65
DB 3 GIGLIDITELKRIASMAGRQKRFARILITRSLDQYELSEKRNKEFLAGRFAAKEAFSA 62
QY 66 MGTGISK-LGFQDLEVLNNEKAPY-----FSQAPFSGKWLISHTDQVTVASVILE 117
DB 63 FGIGIGRLSFDIEIRKQNGKRYIICTKLSQA---AVHVSITHTKEYAAQAQVVI 116
RESULT 15
ABB47581
ID ABB47581 standard; Protein; 118 AA.
XX
AC ABB47581;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #285.
XX
KM Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KM vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusnick C, Reith H, Deboux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunz F, Cossart P;
PI Daniels U, Goebel W, Krefte U, Kuhn M, Ng B, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tellez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.
XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides -

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 19:34:21 ; Search time 21 Seconds
(Without alignments)

245,806 Million cell updates/sec

Title: US-09-897-645-1

Sequence: 1 MMTVGHGIDIEELASIESA.....ISHTDOFVTASVILEBNH 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/6C_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	618	100.0	122 3 US-08-987-144-2	Sequence 2, Appli
2	618	100.0	156 4 US-09-163-446-2	Sequence 2, Appli
3	289	46.8	129 4 US-09-107-532A-6990	Sequence 6990, Ap
4	251	40.6	121 4 US-09-163-446-4	Sequence 4, Appli
5	199.5	32.3	124 4 US-09-134-001C-4274	Sequence 4274, Ap
6	139.5	22.6	126 4 US-08-728-742A-10	Sequence 10, Appl
7	135.5	21.9	122 4 US-09-198-452A-330	Sequence 330, App
8	111.5	18.0	119 4 US-08-728-742A-11	Sequence 11, Appl
9	111.5	18.0	121 4 US-08-728-742A-2	Sequence 2, Appli
10	110	17.8	121 4 US-08-728-742A-3	Sequence 3, Appli
11	107.5	17.4	120 4 US-08-728-742A-1	Sequence 1, Appli
12	107	17.3	122 4 US-08-728-742A-4	Sequence 4, Appli
13	81	13.1	233 4 US-09-328-352-7929	Sequence 7929, Ap
14	80.5	13.0	208 4 US-09-134-001C-3478	Sequence 3478, Ap
15	76	12.3	130 4 US-08-728-742A-8	Sequence 8, Appli
16	74	12.0	130 4 US-08-728-742A-7	Sequence 7, Appli
17	72.5	11.7	371 4 US-09-134-001C-3672	Sequence 3672, Ap
18	72	11.7	169 4 US-09-107-532A-6366	Sequence 6366, Ap
19	71.5	11.6	130 4 US-08-728-742A-5	Sequence 5, Appli
20	71.5	11.6	431 4 US-09-107-532A-7056	Sequence 7056, Ap
21	71.5	11.6	475 4 US-09-252-991A-66219	Sequence 26219, A
22	70.5	11.4	318 3 US-08-680-506-3	Sequence 3, Appli
23	70.5	11.4	449 3 US-08-680-506-7	Sequence 7, Appli
24	70.5	11.4	1052 3 US-09-253-502-7	Sequence 7, Appli
25	70.5	11.4	1052 4 US-09-360-237-1	Sequence 1, Appli
26	70.5	11.4	1052 4 US-09-360-237-3	Sequence 3, Appli
27	68	11.0	113 4 US-09-107-532A-6985	Sequence 6985, Ap

28	66	10.7	176 4 US-09-252-991A-24888	Sequence 24888, A
29	66	10.7	518 4 US-09-134-001C-4348	Sequence 4348, Ap
30	65.5	10.6	348 4 US-09-325-932A-160	Sequence 160, App
31	65.5	10.6	970 6 5229293-2	Patent No. 5229293
32	65	10.5	359 4 US-09-252-991A-21741	Sequence 21741, A
33	64.5	10.4	248 4 US-09-325-932A-161	Sequence 161, App
34	64	10.4	514 4 US-09-252-991A-19394	Sequence 19394, A
35	63.5	10.3	468 4 US-09-166-350-12	Sequence 12, Appl
36	63.5	10.3	412 4 US-09-252-991A-17208	Sequence 17208, A
37	63.5	10.3	592 6 5200183-18	Patent No. 5200183
38	63	10.2	129 4 US-08-728-742A-6	Sequence 6, Appli
39	63	10.2	437 2 US-08-737-716-2	Sequence 2, Appli
40	62.5	10.1	258 4 US-09-328-352-4425	Sequence 4425, Ap
41	62.5	10.1	343 4 US-09-107-532A-6711	Sequence 6711, Ap
42	62.5	10.1	2154 2 US-08-841-349-4	Sequence 4, Appli
43	62	10.0	165 1 US-08-051-142-2	Sequence 2, Appli
44	62	10.0	539 4 US-09-198-452A-543	Sequence 543, App
45	62	10.0	587 1 US-08-844-280-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-08-987-144-2
; Sequence 2, Application US/08987144
; Patent No. 6060282
; GENERAL INFORMATION:
; APPLICANT: Rostek Jr., Paul R.
; TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
; TITLE OF INVENTION: dpy-acaps
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: U.S.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,144
; FILING DATE: December 8, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39, 872
; REFERENCE/DOCKET NUMBER: X-11754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-987-144-2
Query Match 100.0%; Score 618; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.7e-71;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMTVGHGIDIEELASIESAVTRHGFARVLTAGEMERFTSLKGRQIETLAGRWSAKE 60
DB 1 MMTVGHGIDIEELASIESAVTRHGFARVLTAGEMERFTSLKGRQIETLAGRWSAKE 60
QY 61 AFSKMGIGISIKLGRQDIELVNINRGARFYFOAPFSGKTIWISISHTDOFVTASVILEBNH 120
DB 61 AFSKMGIGISIKLGRQDIELVNINRGARFYFOAPFSGKTIWISISHTDOFVTASVILEBNH 120
```

QY 121 ES 122
Db 121 ES 122

RESULT 2

US-09-163-446-2
Sequence 2, Application US/09163446
Patent No. 6515119
GENERAL INFORMATION:
APPLICANT: Frittz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
FILE REFERENCE: 07334/097001
CURRENT APPLICATION NUMBER: US/09/163,446
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 156
TYPE: PR1
ORGANISM: Streptococcus pneumonia
US-09-163-446-2

Query Match 100.0%; Score 618; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 9, 6e-71;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTVGHGIDIEELASISAVTRHGFARVLTQEMERFTSLKGRQIETYLGRWSAKE 60
Db 35 MMTVGHGIDIEELASISAVTRHGFARVLTQEMERFTSLKGRQIETYLGRWSAKE 94
QY 61 AFKAMGTGISKGFQDLEVLNNGRGAPYFSQAPFSGKIWLISHTDQFVTASVIL 120
Db 95 AFKAMGTGISKGFQDLEVLNNGRGAPYFSQAPFSGKIWLISHTDQFVTASVIL 154
QY 121 ES 122
Db 155 ES 156

RESULT 3

US-09-107-532A-6990
Sequence 6990, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucetree-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6990:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium
FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1..129
SEQUENCE DESCRIPTION: SEQ ID NO: 6990:
US-09-107-532A-6990

Query Match 46.8%; Score 289; DB 4; Length 129;
Best Local Similarity 48.3%; Pred. No. 5, 1e-29;
Matches 56; Conservative 21; Mismatches 39; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASISAVTRHGFARVLTQEMERFTSLKGRQIETYLGRWSAKEAF 62
Db 14 MIVGHGIDIEELASISAVTRHGFARVLTQEMERFTSLKGRQIETYLGRWSAKEAF 73
QY 63 SKAMGTGISKGFQDLEVLNNGRGAPYFSQAPFSGKIWLISHTDQFVTASVIL 118
Db 74 SKAMGTGISKGFQDLEVLNNGRGAPYFSQAPFSGKIWLISHTDQFVTASVIL 129

RESULT 4

US-09-163-446-4
Sequence 4, Application US/09163446
Patent No. 6515119
GENERAL INFORMATION:
APPLICANT: Frittz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
FILE REFERENCE: 07334/097001
CURRENT APPLICATION NUMBER: US/09/163,446
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 121
TYPE: PR1
ORGANISM: Streptococcus pneumonia
US-09-163-446-4

Query Match 40.6%; Score 251; DB 4; Length 121;
Best Local Similarity 44.6%; Pred. No. 3, 2e-24;
Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;

QY 3 MIVGHGIDIEELASISAVTRHGFARVLTQEMERFTSLKGRQIETYLGRWSAKEAF 62
Db 1 MIVGHGIDIEELASISAVTRHGFARVLTQEMERFTSLKGRQIETYLGRWSAKEAF 60
QY 63 SKAMGTGISKGFQDLEVLNNGRGAPYFSQAPFSGKIWLISHTDQFVTASVIL 116
Db 61 SKAMGTGISKGFQDLEVLNNGRGAPYFSQAPFSGKIWLISHTDQFVTASVIL 116
QY 117 E 117
Db 117 E 117

RESULT 5

US-09-134-001C-4274

; Sequence 4274, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lyon Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4274
; LENGTH: 124
; TYPE: PR1
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4274

Query Match 32.3%; Score 199.5; DB 4; Length 124;
Best Local Similarity 37.2%; Pred. No. 1,2e-17;
Matches 45; Conservative 30; Mismatches 41; Indels 5; Gaps 4;

QY 1 MMTVHGIDIEELASISAVTRH-EGPAKRVLTAAQEMERTSLKGRQIEYLAGRMSAK 59
DB 6 IGVYIGIDIEELASISAVTRH-EGPAKRVLTAAQEMERTSLKGRQIEYLAGRMSAK 64
QY 60 EAFSKAMGTGISK-LGFDQDEVLNNGRGAPYFSQAPFSQKIMWLSISHTDQFVTASVI 118
DB 65 EAFSKAMGTGISKVSQDINCNDALGKRCIDYPPGYTHV-SIHTEHYAMSVITLAK 122
QY 119 N 119
DB 123 N 123

RESULT 6
US-08-728-742A-10
; Sequence 10, Application US/08728742A
; Patent No. 6579695
; GENERAL INFORMATION:
; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
; TITLE OF INVENTION: PHOSPHOPANTHETHEINYL TRANSFERASES AND USES THEREOF
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS: 78
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,742A
; FILING DATE: October 11, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,152
; FILING DATE: October 13, 1995
; APPLICATION NUMBER: 60/021,650
; FILING DATE: July 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: HMI-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-728-742A-10

Query Match 22.6%; Score 139.5; DB 4; Length 126;
Best Local Similarity 30.3%; Pred. No. 5.1e-10;
Matches 40; Conservative 26; Mismatches 39; Indels 27; Gaps 5;

QY 4 IGVHGIDIEELASISAVTRH-EGPAKRVLTAAQEMERTSLKGRQIEYLAGRMSAKAF 62
DB 3 ILGLGTDIVEIARIEAVIARSGDRLARRVLSDNEMAIWKT-HHQPVAFLLAKFAVKEAA 60
QY 63 SKAMGTGI-SKLGFDQDEVLNNGRGAPYFSQAPFSQKIMWLSISHTDQFVTASVI 105
DB 61 AKAFGTGIRNGLAIFQEFVFNDELGKPRL-----KLNGERALKLAEKLVANMHVTLAD 113
QY 106 TDQFVTASVILE 117
DB 114 BRHVACATVITE 125

RESULT 7
US-09-198-452A-330
; Sequence 330, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 330
; LENGTH: 122
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-330

Query Match 21.9%; Score 135.5; DB 4; Length 122;
Best Local Similarity 35.3%; Pred. No. 1.6e-09;
Matches 42; Conservative 19; Mismatches 49; Indels 9; Gaps 5;

QY 4 IGVHGIDIEELASISAVTRH-EGPAKRVLTAAQEMERTSLKGRQIEYLAGRMSAKAF 62
DB 3 IHTGTDLIEISRIKREAIATGNRLNRIFT--EAEQKCYCLEKTPPIPSFACRPAKRAV 60
QY 63 SKAMGTGI-SKLGFDQDEVLNNGRGAPYFSQAPFSQKIMWLSISHTDQFVTASVI 115
DB 61 AKALGTGIGSVVAMWDIEVFVKSHQPEVLLPSHVYAKIGISKVILISHCKEYATATAT 119

RESULT 8
US-08-728-742A-11
; Sequence 11, Application US/08728742A
; Patent No. 6579695
; GENERAL INFORMATION:
; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
; TITLE OF INVENTION: PHOSPHOPANTHETHEINYL TRANSFERASES AND USES THEREOF
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS: 78
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:

ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMT-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-728-742A-2

Query Match 18.0%; Score 111.5; DB 4; Length 121;
Best Local Similarity 32.5%; Pred. No. 1.8e-06;
Matches 40; Conservative 22; Mismatches 40; Indels 21; Gaps 8;

D6 GHGDIIEELASAVTRHEGFARVLTQEMERFTSLKRRQLEYLAGRNSAKEAFSKA 65
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
2 GGVADVVELTISIN--VENDTFIERNFTQGLE-YCSAQSVSSF-AGTWSAAEAVFKS 56
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
D6 66 MGTSIKLGL---FDLDLVNNRGAPYF-----SQAPFSG--KIWLISHTD-QPVT 111
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
D6 57 L-GVKSLGGGALKKDIELVRNKKNPAVPELVHGNATKAALAEAGVTDVXYSISHDDLQA 114
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 112 ASV 114
:|
DB 115 VAV 117

RESULT 10
US-08-728-742A-3
Sequence 3, Application US/08728742A
Patent No. 6579695
GENERAL INFORMATION:
APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
TITLE OF INVENTION: PHOSPHOPATE THEINYL TRANSFERASES AND USES THEREOF
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMT-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear

```

QY      6 GHGDIIEIASIESAVRRHESFAKRVLTQAOMSEFTSLKKGRQIETLYAGRSASAKAEBSKA   65
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     2 GVGVDVALLSAIN---IDNEFFIERNTGNVEF--YCINTAHPPQASTGTGLTSAKEAIVKRA   56
QY      66 MCGICISLKGQC-DLEVLNNGRGAPYF-----SQAPFSG-XIWTSISHTPDFOVTASY    114
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
57 LVSCKSGAGSLIDIELTRPVNGPKVIHLHGAAKKAAGAAGVKVNIIISIH-DFEOATAY    115

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?  APPLICANT: Gary L. Breton et al.
?  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
?  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
?  FILE REFERENCE: GTC99-03PA
?  CURRENT APPLICATION NUMBER: US/09/328,352
?  CURRENT FILING DATE: 1999-06-04

```

NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7929
LENGTH: 233
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7929

Query Match 13.1%; Score 81; DB 4; Length 233;
Best Local Similarity 35.1%; Pred. No. 0.035;
Matches 27; Conservative 7; Mismatches 33; Indels 10; Gaps 3;

QY 8 GIDIEELASIESAVTRHEGFAKRVLTQEMERFTSLKGRQIEYLAGWSAKAEASKANG 67
DB 112 GIDVEEL---DRKVRLDLSLOHAFHPDEYATWQSLQDR--EYWFVWTTKEAVLKASG 165

QY 68 TGISKLGFDLEVINNE 84
DB 166 LGIR---LDLNTLNTQ 178

RESULT 14
US-09-134-001C-3478
Sequence 3478, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3478
LENGTH: 208
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3478

Query Match 13.0%; Score 80.5; DB 4; Length 208;
Best Local Similarity 30.8%; Pred. No. 0.034;
Matches 24; Conservative 15; Mismatches 26; Indels 13; Gaps 4;

QY 8 GIDIEELASIESAVTRHEGFAKRVLTQEMERFTSLKGRQIEYLAGWSAKAEASKANG 67
DB 105 GIDIEEKQID-----YKHLAKN-FTQNEPNOVTTLKDFYEI-----WTKESYTKLIG 152

QY 68 TGISKLGFDLEVINNE 85
DB 153 EGLMN-GLDCYDVTONLR 169

RESULT 15
US-08-728-742A-8
Sequence 8, Application US/08728742A
Patent No. 6579695
GENERAL INFORMATION:
APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
TITLE OF INVENTION: PHOSPHORANTHRAHYL TRANSFERASES AND USES THEREOF
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-728-742A-8

Query Match 12.3%; Score 76; DB 4; Length 130;
Best Local Similarity 32.8%; Pred. No. 0.064;
Matches 21; Conservative 7; Mismatches 30; Indels 6; Gaps 1;

QY 8 GIDIEELASIESAVTRHEGFAKRVLTQEMERFTSLKGRQIEYLAGWSAKAEASKANG 67
DB 11 GIDIEKTKPISLEI-----AKRFKTEVSDLLAKXKDQTDYFYLMGKESFIQEG 64

QY 68 TGIS 71
DB 65 KGLS 68

Search completed: December 10, 2003, 19:37:30
Job time: 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 19:33:16 ; Search time 20 Seconds
(without alignments)
586.629 Million cell updates/sec

Title: US-09-897-645-1

Perfect score: 618

Sequence: 1 MNMIVGHGIDIEELASIESA.....ISHTDQFVTAASVILENNHS 122

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608	98.4	120	2	H95197
2	608	98.4	120	2	D98064
3	302	48.9	119	2	C86730
4	279	45.1	119	2	F83714
5	251	40.6	121	1	H69772
6	233	37.7	118	2	AE1185
7	228	36.9	118	2	AD1543
8	208	33.7	119	2	E89999
9	187.5	30.3	126	2	F82072
10	181	29.3	126	2	F71662
11	172.5	27.9	169	2	B73445
12	171	27.7	131	2	A97810
13	169.5	27.4	124	2	B66960
14	161.5	24.5	125	2	D81833
15	149.5	24.2	126	2	AG0828
16	148.5	24.0	126	2	E91057
17	148.5	24.0	126	2	B85902
18	146.5	23.7	125	2	F81197
19	145.5	23.5	126	2	F84959
20	140	22.7	125	2	F71276
21	139.5	22.6	126	1	B42294
22	137.5	22.2	126	2	AF0356
23	135.5	21.9	122	2	D90789
24	135.5	21.9	122	2	A86530
25	135.5	21.9	122	2	B72003
26	135.5	21.9	122	2	G86649
27	133	21.5	115	2	A81286
28	128.5	20.8	115	2	G82895
29	125.5	20.3	119	2	C71556

30	125.5	20.3	191	2	AC3413	holo-[acyl-carrier
31	123	19.9	119	1	S73864	hypothetical prote
32	122.5	19.8	134	2	AH2703	holo-[acyl-carrier
33	122.5	19.8	134	2	H97485	holo-[acyl-carrier
34	121.5	19.7	119	1	H64620	holo-[acyl-carrier
35	117.5	19.0	119	2	G71894	holo-[acyl-carrier
36	113	18.3	124	2	B70101	holo-[acyl-carrier
37	111.5	18.0	125	2	D81710	holo-[acyl-carrier
38	111.5	18.0	1887	2	S61703	holo-[acyl-carrier
39	110	17.8	1857	1	S01787	fatly-acid synthas
40	109	17.6	133	2	F75544	fatly-acid synthas
41	108.5	17.6	133	2	E87442	probable holo-acyl
42	108	17.5	123	2	F35573	holo-[acyl-carrier
43	107.5	17.4	1885	1	JC4086	probable holo-acyl
44	107	17.3	377	2	T43037	fatly-acid synthas
45	107	17.3	1842	2	T43409	probable fatly-aci

ALIGNMENTS

RESULT 1
H95197
holo-[acyl-carrier protein] synthase [imported] - Streptococcus pneumoniae (strain TIG
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C/Accession: H95197
R/Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; He
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morriso
A/Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:2157209; PMID:11463916
A/Accession: H95197
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-120 <KUR>
A/Cross-references: GB:AE005672; PIDN:AAK75777.1; PID:g14973193; GSPDB:GN00164; TIGR:S
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SPI699
C/Superfamily: holo-ACP synthase

Query Match 98.4%; Score 608; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 8.3e-56;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAEQMERFTSLKGRQIEYLGRMSAKAF 62
DB 1 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAEQMERFTSLKGRQIEYLGRMSAKAF 60
QY 63 SKAMGTGTSKGFQDLVNNRGAAPYSPQAFSGKIMVISHHTDQFVTAASVILENNHS 122
DB 61 SKAMGTGTSKGFQDLVNNRGAAPYSPQAFSGKIMVISHHTDQFVTAASVILENNHS 120

RESULT 2
D98064
holo-[acyl-carrier protein] synthase (EC 2.7.8.7) [imported] - Streptococcus pneumonia
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C/Accession: D98064
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burger, S.; Dehoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Letkowitz, E.J.; Lu, U.; Matsushima, P.; McAnen, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: D98064
A/Status: preliminary
A/Molecule type: DNA

A;Residues: 1-120 <KUN>
A;Cross-references: GB:AE007317, PIDN:AA100345.1, PID:g15459205, GSPDB:GN00174
C;Genetics: acps
A;Gene: acps
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A, transferase

Query Match 98.4%; Score 608; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 8.3e-56;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 62
DB 1 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 60
QY 63 SKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 122
DB 61 SKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 120

RESULT 3
C86730
acyl carrier protein synthase [imported] - Lactococcus lactis subsp. lactis (strain IL14)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: C86730
R;Bolotin, A.; Wincker, P.; Manger, S.; Dailon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, S.D.;
G. Bolo, R., 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp.
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: GB:AE005176; PID:g12723769; PIDN:AAK04941.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics: acps
A;Gene: acps
C;Superfamily: holo-ACP synthase

Query Match 48.9%; Score 302; DB 2; Length 119;
Best Local Similarity 51.3%; Pred. No. 4.1e-24;
Matches 61; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

QY 3 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 61
DB 1 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 60
QY 62 FSKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 119
DB 61 FSKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 119

RESULT 4
F83714
holo-(acyl carrier protein) synthase BH0518 [imported] - Bacillus halodurans (strain C-1)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83714
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:DBA04237.1; GSPDB:GN00
C;Experimental source: strain C-125
A;Gene: BH0518
C;Superfamily: holo-ACP synthase

Query Match 45.1%; Score 279; DB 2; Length 119;
Best Local Similarity 52.6%; Pred. No. 9.9e-22;
Matches 61; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

QY 3 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 62
DB 1 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 60
QY 63 SKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 117
DB 61 SKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 115

RESULT 5
H69772
holo-(acyl-carrier-protein) synthase (EC 2.7.8.7) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: H69772
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni, E.
C.; Bron, S.; Brouillet, S.; Brunelle, C.V.; Caillet, B.; Capuano, V.; Carter, N.M.; C.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallizzi, A.;
Iech, J.; Harwood, C.R.; Hentz, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lander, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masui, N.; Maue,
Y. M.; Ogawa, K.; Ogata, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portetel,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlan,
A;Authors: Schleith, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Ser,
Akenuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A;Reference number: A69580; MUID:98044035; PMID:9384377
A;Accession: H69772
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-121 <KUN>
A;Cross-references: GB:Z99106; GB:AL009126; NID:g2632653; PIDN:CB12269.1; PID:g263276
A;Experimental source: strain 168
C;Genetics: ydcB
A;Gene: ydcB
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A, transferase

Query Match 40.6%; Score 251; DB 1; Length 121;
Best Local Similarity 44.6%; Pred. No. 8e-19;
Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;

QY 3 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 62
DB 1 MIVGHGIDIELASIESAVTRHGFARVLTAAQEMERTSLKGRQIEYLAGRMSAKEAF 60
QY 63 SKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 116
DB 61 SKAMGTGISKLGFDLEVINNRGAPYFSGAKIMLSISHTDQFVTAIVLENNES 116
QY 117 E 117
DB 117 E 117

RESULT 6
AE1185
holo-acyl-carrier protein synthase hm0085 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AE1185
R;Glasier, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baguer, F.; Berche, P.; Bloech,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A.; Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; PMID:11679669
A:Accession: AB1185
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC98963.1; PID:g16410288; GSPDB:GN00177
A:Experimental source: strain EGD-8
C:Genetics:
A:Gene: lmo0885
C:Superfamily: holo-ACP synthase

Query Match 37.7%; Score 233; DB 2; Length 118;
Best Local Similarity 42.7%; Pred. No. 5.7e-17;
Matches 50; Conservative 30; Mismatches 35; Indels 2; Gaps 2;

QY 3 MIVGHGIDIEELASISAVTRHGFPAKRVLTQEMERFTSLKGRQIEYLAGWSAKAP 62
DB 1 MTHGIGLDWIDLRVQVKNRFRTERVLTKEIKQFEKYNRIEFLAGRFPAKAY 60

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 117
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 117

RESULT 7

AD1543
holo-acyl-carrier protein synthase homolog lin0884 [imported] - *Listeria innocua* (strain
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

A:Accession: AD1543
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entlian, K.D.; Fshih, H.
Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A.; Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; PMID:11679669
A:Accession: AD1543
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96116.1; PID:g16413334; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin0884
C:Superfamily: holo-ACP synthase

Query Match 36.9%; Score 228; DB 2; Length 118;
Best Local Similarity 40.7%; Pred. No. 1.9e-16;
Matches 48; Conservative 32; Mismatches 36; Indels 2; Gaps 2;

QY 3 MIVGHGIDIEELASISAVTRHGFPAKRVLTQEMERFTSLKGRQIEYLAGWSAKAP 62
DB 1 MTHGIGLDWIDLRVQVKNRFRTERVLTKEIKQFEKYNRIEFLAGRFPAKAY 60

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 118
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 118

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 118
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 118

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 118
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 118

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 118
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 118

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 118
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 118

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 118
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 118

QY 63 SKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 118
DB 61 AKANGTGFQKHLSTFDVETLQVEDGRPHVTLTPVKSSENVFVSTHTARSAAGVILE 118

Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of metcillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; PMID:12131952; PMID:11418146
A:Accession: E89999
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-119 <KUR>
A:Cross-references: GB:BA000018; PID:g13701866; PIDN:BA843158.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: dpj
C:Superfamily: holo-ACP synthase

Query Match 33.7%; Score 208; DB 2; Length 119;
Best Local Similarity 37.8%; Pred. No. 2.2e-14;
Matches 45; Conservative 29; Mismatches 41; Indels 4; Gaps 3;

QY 3 MIVGHGIDIEELASISAVTRHGFPAKRVLTQEMERFTSLKGRQIEYLAGWSAKAP 61
DB 1 MTHGIGVDLIEIDRIKVLKSKPKLVERILTQNEOKFNFTHEOKRIEFLAGRFPAKAY 60

QY 62 FSKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-TWLSISHTDQFVTASVILE 119
DB 61 FSKALGTGKHAFAFNDICVDELSKPKIDYEGFT--VHVSISHTHEVAMSVVLEKS 117

RESULT 9

F82072
holo-acyl-carrier-protein synthase VC2457 [imported] - *Vibrio cholerae* (strain N1696
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

A:Accession: F82072
R:Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoli, I.; Sellers,
L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; PMID:120406833; PMID:10952301
A:Accession: F82072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <HEI>
A:Cross-references: GB:AE004316; GB:AE003852; NID:g9657034; PIDN:AAF95599.1; GSPDB:GNO
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2457
A:Map position: 1
C:Superfamily: holo-ACP synthase

Query Match 30.3%; Score 187.5; DB 2; Length 126;
Best Local Similarity 40.3%; Pred. No. 3.2e-12;
Matches 52; Conservative 23; Mismatches 35; Indels 19; Gaps 5;

QY 3 MIVGHGIDIEELASISAVTRH-EGFAKRVLTQEMERFTSLKGRQIEYLAGWSAKAP 61
DB 1 MIVGHGIDIEELASISAVTRH-EGFAKRVLTQEMERFTSLKGRQIEYLAGWSAKAP 61

QY 62 FSKAMGTGISK-LGFODLEVLNNEGAPYFSQAPFSGK-----TWLSISHTDQ 108
DB 59 ASKALGTGAGVWTHDFTISHDKLGKPLLT--LSQAAELIASQLQVENHILISDERH 115

QY 109 FVTASVILE 117
DB 116 YAMATVILE 124

QY 109 FVTASVILE 117
DB 116 YAMATVILE 124

QY 109 FVTASVILE 117
DB 116 YAMATVILE 124

QY 109 FVTASVILE 117
DB 116 YAMATVILE 124

QY 109 FVTASVILE 117
DB 116 YAMATVILE 124

QY 109 FVTASVILE 117
DB 116 YAMATVILE 124

QY 109 FVTASVILE 117
DB 116 YAMATVILE 124

holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) NMA2033 [imported] - *Neisseria meningitidis*

C:/Species: Neisseria meningitidis
C:/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:/Accession: D81833
R:/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,
H.; Holroyd, S.; Jørgensen, K.; Leach, S.; Mouton, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:/Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:/Reference number: A81775; MUID:2022556; PMID:10761919
A:/Accession: D81833
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-125 <PAR>
A:/Cross-references: GB:AL162757; GB:AL157959; NID:97380371; PIDN:CAM85252.1; PID:9738066
A:/Experimental source: serogroup A, strain Z2491
A:/Genetics: acps; NMA2033
C:/Superfamily: holo-ACP synthase
C:/Keywords: coenzyme A; transferase

Query Match 24.5%; Score 151.5; DB 2; Length 125;
Best Local Similarity 33.3%; Pred. No. 1.7e-08;
Matches 43; Conservative 25; Mismatches 46; Indels 13; Gaps 4;

QY 3 MIVGHGIDIDELASISAVTRH-EGFAKRVLTAEEMERFTSLKGRQIEYIAGRSAXEA 61
DB 1 MIVGHGIDIVSLKRIVRLSKPGQAFARILITPELEFFP--QAGKPVNVLAKRFAKXA 58
QY 62 FSKAMGTGT-SKLGFQDLEVLNNRGAAPYSGAPFSGK-----TWLSISHTDQFVT 111
DB 59 FAKAVGTGIRGAVFNRNIGIGHDALGKPEFFVAPALSKMLEEQISRSVLSMSDEDETVL 118
QY 112 ASVILEE 118
DB 119 AFAVAER 125

RESULT 15

AG0828
holo-lacyl-carrier protein synthase (EC 2.7.8.7) [imported] - *Salmonella enterica* subsp.
C:/Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A:/Note: this species has also been called *Salmonella typhi*
C:/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:/Accession: AG0828
R:/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th. T.; Connor, P.; Cronin, A.; Davis, P.; Davies, K.M.; Dowd, L.; White, N.; Farrar,
S.; Mouton, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:/Reference number: AB0502; MUID:21534947; PMID:11677608
A:/Accession: AG0828
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-126 <PAR>
A:/Cross-references: GB:AL153382; PIDN:CAD02779.1; PID:916503789; GSPDB:GN00176
C:/Genetics:
A:/Gene: STY2823
C:/Superfamily: holo-ACP synthase
C:/Keywords: coenzyme A; transferase

Query Match 24.2%; Score 149.5; DB 2; Length 126;
Best Local Similarity 33.3%; Pred. No. 2.8e-08;
Matches 44; Conservative 24; Mismatches 37; Indels 27; Gaps 6;

QY 4 IVGHGIDIDELASISAVTRH-EGFAKRVLTAEEMERFTSLKGRQIEYIAGRSAXEA 62
DB 3 IIVGHGIDIVSLKRIVRLSKPGQAFARILITPELEFFP--QAGKPVNVLAKRFAKXA 60
QY 63 SKAMGTGT-SKLGFQDLEVLNNRGAAPYSGAPFSGK-----TWLSISHTDQFVT 107
DB 61 AKAFGTGIRGAVFNRNIGIGHDALGKPEFFVAPALSKMLEEQISRSVLSMSDEDETVL 113
QY 108 --QFVAVILE 117

DB 114 ERHYACFVILE 125
Search completed: December 10, 2003, 19:36:56
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 19:32:01 ; Search time 13 Seconds
(without alignments)
441.328 Million cell updates/sec

Title: US-09-897-645-1
Perfect score: 618
Sequence: 1 MRMIVGHGIDIEELASIESA.....ISHTDPVTASVILENHES 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	608	98.4	120	1	ACPS_STRPN
2	397	64.2	119	1	ACPS_STRMU
3	339	54.9	118	1	ACPS_STRP3
4	339	54.9	118	1	ACPS_STRPY
5	328.5	53.2	119	1	ACPS_STRA3
6	302	48.9	119	1	ACPS_STRA1
7	279	45.1	119	1	ACPS_STRAC
8	278.5	45.1	119	1	ACPS_STRAD
9	251	40.6	121	1	ACPS_STRAE
10	233	37.7	118	1	ACPS_STRAM
11	228	36.9	118	1	ACPS_STRAN
12	221	35.8	117	1	ACPS_STRAP
13	212	34.3	119	1	ACPS_STRAR
14	210.5	34.1	126	1	ACPS_STRAU
15	208	33.7	119	1	ACPS_STRAV
16	199.5	32.3	117	1	ACPS_STRAW
17	196.5	32.3	122	1	ACPS_STRAX
18	196.5	31.8	117	1	ACPS_STRAY
19	195.5	31.6	126	1	ACPS_STRAZ
20	189.5	30.7	133	1	ACPS_STRBA
21	187.5	30.3	126	1	ACPS_STRBB
22	181	29.3	126	1	ACPS_STRBC
23	176	28.5	139	1	ACPS_STRBD
24	172.5	27.9	169	1	ACPS_STRBE
25	171	27.7	131	1	ACPS_STRBF
26	169.5	27.4	124	1	ACPS_STRBG
27	159.5	25.8	126	1	ACPS_STRBH
28	158.5	25.6	127	1	ACPS_STRBI
29	151.5	24.5	125	1	ACPS_STRBJ
30	150.5	24.4	127	1	ACPS_STRBK
31	149.5	24.2	125	1	ACPS_STRBL
32	148.5	24.0	125	1	ACPS_STRBM
33	148.5	24.0	125	1	ACPS_STRBN

34	149.5	24.0	128	1	ACPS_STRBP	P59475 buchnera ap
35	147	23.8	114	1	ACPS_MYCE	Q92b79 mycoplasma
36	146.5	23.7	125	1	ACPS_NEIMB	Q9rml8 neisseria m
37	145.5	23.5	126	1	ACPS_BUCAI	P57344 buchnera ap
38	140	22.7	125	1	ACPS_TREPA	O83800 treponema p
39	139.5	22.6	125	1	ACPS_ECOLI	P24224 escherichia
40	138.5	22.4	137	1	ACPS_RHILU	Q965a8 rhizobium l
41	137.5	22.2	126	1	ACPS_YERPE	O82c35 yersinia pe
42	135.5	21.9	122	1	ACPS_CHLJP	Q928m5 chlamydia p
43	135.5	21.9	122	1	ACPS_ECO57	O8xan7 escherichia
44	133	21.5	115	1	ACPS_CAMYE	Q9pmp8 campylobact
45	128.5	20.8	115	1	ACPS_UREPA	Q9p97 ureaplasma

ALIGNMENTS

RESULT 1	ACPS_STRPN	STANDARD;	PRT;	120 AA.
AC	Q9F7T5;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Holo-lacyl-carrier protein synthase (EC 2.7.8.7) (Holo-ACP synthase)			
DE	(4'-phosphopantetheinyl transferase acps).			
GN	ACPS OR SP1699 OR SPRI541.			
OS	Streptococcus pneumoniae, and			
OS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1313, 171101;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC BAA-255 / R6;			
RX	MEDLINE=20469436; PubMed=10903317;			
RA	McAllister K.A., Peery R.B., Weyer T.I., Fischl A.S., Zhao G.,			
RT	"Biochemical and molecular analyses of the streptococcus pneumoniae			
RT	acyl carrier protein synthase, an enzyme essential for fatty acid			
RT	biosynthesis."			
RL	J. Biol. Chem. 275:30864-30872(2000).			
RP	[2]			
RC	SEQUENCE FROM N.A.			
RX	STRAIN=ATCC BAA-334 / TIGR4;			
RX	MEDLINE=21357209; PubMed=11463916;			
RA	Peterson S., Heideberg J., Deboy R.T., Bisen J.A., Read T.D.,			
RA	Durkin A.S., Grimm M., Kolonay J.F., Nelson W.C., Peterson J.D.,			
RA	Umayam L.A., White O., Salzberg S.L., Uterback T.R., Hansen C.L.,			
RA	Holtapfel E., Kouri H., Wolf A.M., Uterback T.R., Hansen C.L.,			
RA	McDonald L.A., Feldblyum T.V., Angiuoli S., Dickenson T., Hickey E.K.,			
RA	Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,			
RA	Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,			
RT	"Complete genome sequence of a virulent isolate of Streptococcus			
RT	pneumoniae."			
RL	Science 293:498-506(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC BAA-255 / R6;			
RX	MEDLINE=21429245; PubMed=11544234;			
RA	Hoskins J., Aldrem W.E. Jr., Arnold J., Blaszcak L.C., Bargett S.,			
RA	DeHoff B.S., Bstrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,			
RA	Gilmour R.J., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,			
RA	LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsumura P.,			
RA	McLaren S.M., McMeney M., Mcleaster K., Mundy C.W., Niclas T.I.,			
RA	Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,			
RA	Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,			
RA	Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,			
RT	Glass J.I.;			
RT	"Genome of the bacterium Streptococcus pneumoniae strain R6."			
RL	J. Bacteriol. 183:5709-5717(2001).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH 3'-5'-ADP.			

```

RX MEDLINE=20490359; PubMed=11032795;
RA Chirgadze N.Y., Briggs S.L., McAllister K.A., Fischl A.S., Zhao G.;
RT "Crystal structure of streptococcus pneumoniae acyl carrier protein
synthase: an essential enzyme in bacterial fatty acid biosynthesis.";
RL EMO J. 19:5281-5287(2000).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
FAMILY.
CC -----
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CC -----
DR EMBL: AF276617; AAC22706.1; -
DR EMBL: AE007463; AAT75777.1; -
DR EMBL: AE008522; AAL00345.1; -
DR PIR: D98064; D98064.
DR PIR: H95197; H95197.
DR PDB: 1FTE; 12-SEP-01.
DR PDB: 1FTF; 12-SEP-01.
DR PDB: 1FTH; 12-SEP-01.
DR TIGR: SP1699; -.
DR HAMAP: MF_00101; -.
DR InterPro: IPR004582; ACPS.
DR InterPro: IPR004568; Pantethn_tm.
DR Pfam: PF01648; ACPS.1.
DR ProDom: PD004282; ACPS.1.
DR TIGRFAMs: TIGR00516; acps.1.
DR TIGRFAMs: TIGR00556; pantethn_tm.1.
DR Transferrase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KM 3D-structure; Complete proteome.
FT METAL 8 58 MAGNESIUM (BY SIMILARITY).
FT METAL 58 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 120 AA; 1338 MW; 7FFB1848AC6DABE CRC64;

Query Match 98.4%; Score 608; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.1e-54;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIVGHGIDIBELASISAVTRHGFARVLTQEMERFTSLKGRQIEYLAGRWSAKAF 62
DB 1 MIVGHGIDIBELASISAVTRHGFARVLTQEMERFTSLKGRQIEYLAGRWSAKAF 60
QY 63 SKAMGTGISTLGFQDLEVLNNERGAFFSQAPFSGKIMLSISTDQFVTASVILEENH 122
DB 61 SKAMGTGISTLGFQDLEVLNNERGAFFSQAPFSGKIMLSISTDQFVTASVILEENH 120

RESULT 2
ACPS_STRMU STANDARD; PRT; 119 AA.
AC QSDSF3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR SMU.1835.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., Mcshan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson W.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
FAMILY.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE015010; AAN59458.1; -
DR HAMAP: MF_00101; -.
DR Pfam: PF01648; ACPS.1.
DR ProDom: PD004282; ACPS.1.
DR TIGRFAMs: TIGR00516; acps.1.
DR TIGRFAMs: TIGR00556; pantethn_tm.1.
DR Transferrase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KM Complete proteome.
FT METAL 8 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13218 MW; 450139C210FEF866 CRC64;

Query Match 64.2%; Score 397; DB 1; Length 119;
Best Local Similarity 62.7%; Pred. No. 7e-33;
Matches 74; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 3 MIVGHGIDIBELASISAVTRHGFARVLTQEMERFTSLKGRQIEYLAGRWSAKAF 62
DB 1 MIVGHGIDIDIAAIVORAHRSRSRFSKVLTFKLEIFTSLKGRQIEYLAGRWSAKAF 60
QY 63 SKAMGTGISTLGFQDLEVLNNERGAFFSQAPFSGKIMLSISTDQFVTASVILEENH 120
DB 61 SKAMGTGISTLGFQDLEVLNNERGAFFSQAPFSGKIMLSISTDQFVTASVILEENH 118

RESULT 3
ACPS_STRP3 STANDARD; PRT; 118 AA.
AC QSDZF3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR SPW3.1564 OR SP80303 OR SPW18.1872.
OS Streptococcus pyogenes (serotype M3), and
OC Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466, 186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGA315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.;

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RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SSI-1 / Serotype M3;
 RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
 RA Yamaoka K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
 RA Hayaishi H., Hamada S.;
 RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
 RT of S. pyogenes SSI-1, SF370 and MGAS8232";
 RN Submitted (May-2002) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108;
 RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.W., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasey L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a set of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
 CC FAMILY.

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DR EMBL, AE014166; AAM80171.1; -;
 DR EMBL, AP06142; BAC63398.1; -;
 DR EMBL, AE010093; AAL98380.1; -;
 DR HAMAP, MF_00101; -; 1.
 DR InterPro, IPR002582; ACPS.
 DR InterPro, IPR004568; Pantethn_tm.
 DR Pfam, PF01648; ACPS; 1.
 DR ProDom, PD004282; ACPS; 1.
 DR TIGRFAMs, TIGR00516; acps; 1.
 DR TIGRFAMs, TIGR00556; pantethn_tm; 1.
 KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KW Complete proteome.
 FT METAL 8
 FT METAL 58
 SEQUENCE 118 AA, 13262 MW, 54FE6F77EB64BDC CRC64;

Query Match 54.9%; Score 339; DB 1; Length 118;
 Best Local Similarity 53.4%; Pred. No. 4.3e-27;
 Matches 62; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESATVTRHEGPAKRVLTQEMERFTSLKGRQIEVLAGMSAKKAF 62
 DB 1 MIVGHGIDIEELASIESATVTRHEGPAKRVLTQEMERFTSLKGRQIEVLAGMSAKKAF 60
 QY 63 SKAMGTGISKGFQDLEVLNNGRGA PYFSAQPFSGKIMVISHTOQFVTAATLE 118
 DB 61 AKATGTGIGRLTFQDIEILNDVRGCPILTSPFKNSFISHSNGVAVASVILED 116

RESULT 4

ACPS_STRPY
 ID ACPS_STRPY STANDARD; PRT; 118 AA.
 AC 099y97;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS OR SPY1804.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1314;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferrer J.J., McShan W.N., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Natar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a set of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
 CC FAMILY.

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DR EMBL, AE006607; AAK34533.1; -;
 DR HAMAP, MF_00101; -; 1.
 DR InterPro, IPR002582; ACPS.
 DR InterPro, IPR004568; Pantethn_tm.
 DR Pfam, PF01648; ACPS; 1.
 DR ProDom, PD004282; ACPS; 1.
 DR TIGRFAMs, TIGR00516; acps; 1.
 DR TIGRFAMs, TIGR00556; pantethn_tm; 1.
 KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KW Complete proteome.
 FT METAL 8
 FT METAL 58
 SEQUENCE 118 AA, 13269 MW, C3B45CEB64ACSD CRC64;

Query Match 54.9%; Score 339; DB 1; Length 118;
 Best Local Similarity 53.4%; Pred. No. 4.3e-27;
 Matches 62; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESATVTRHEGPAKRVLTQEMERFTSLKGRQIEVLAGMSAKKAF 62
 DB 1 MIVGHGIDIEELASIESATVTRHEGPAKRVLTQEMERFTSLKGRQIEVLAGMSAKKAF 60
 QY 63 SKAMGTGISKGFQDLEVLNNGRGA PYFSAQPFSGKIMVISHTOQFVTAATLE 118
 DB 61 AKATGTGIGRLTFQDIEILNDVRGCPILTSPFKNSFISHSNGVAVASVILED 116

RESULT 5
 ACPS_STRPY3 STANDARD; PRT; 119 AA.
 ID ACPS_STRPY3 STANDARD; PRT; 119 AA.
 AC 08E3M8; 08DY09;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)

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DE 15-SEP-2003 (Rel. 42, Last annotation update)
DI Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DR (4'-phosphopantetheinyl transferase acps).
DE ACPS OR GBS1729 OR SAG1685.
OS Streptococcus agalactiae [serotype III], and
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
OX NCBI_TaxID=216495, 216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaeser P., Rusnick C., Buchrieser C., Chevalier F., Franzen L.,
RA Masadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222968; PubMed=12200547;
RA Tetzelin H., Maissigant V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carthy H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Jacobini E.T., Brettoni C., Galli G., Mariani M., Vegni R., Malone D.,
RA Riando D., Rappunoi R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
CC - FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a set of acyl-carrier protein [By similarity].
CC - CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC - COFACTOR: Magnesium (By similarity).
CC - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC - SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
-----
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-----
CC EMBL, AL766852; CAD47388.1; -
CC DR EMBL, AE014268; AA00549.1; -
CC Sagallast; gbs1729; -.
CC DR TIGR; SAG1685; -.
CC DR HAMAP; MF_00101; -: 1.
CC DR Pfam; PF01648; ACPS; 1.
CC DR ProDom; PD004282; ACPS; 1.
CC DR TIGRFAMs; TIGR00516; acps; 1.
CC DR TIGRFAMs; TIGR00556; pantechn.tn; 1.
CC KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
CC Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 59 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13268 MW; COEEB77DM27CCE2E CRC64;

```

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Db      1 MIVHGIDLDIGAEITAYVERNQFARVILTEGELLFLFKGISNPKRQMSFLTGRMAKEA 60
Oy      62 FSKAMGTGICSLGFODLEVLANNERGAPYFSQAPPSCIKMWSIHTDQFTVASVILEE 118
        :|||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 YSKALGTGIGKVFHDIIEILLSDDGAPLFIETEPENKSFVISHSISGNVAQASVILLE 117

RESULT 6
ACPS_LACTA ID ACPS_LACTA STANDARD; PRT; 119 AA.
AC          Q9CH95;
DT          16-OCT-2001 (Rel. 40, Created)
DT          16-OCT-2001 (Rel. 40, Last sequence update)
DE          28-FEB-2003 (Rel. 41, Last annotation update)
DE          Holo-lacyl-carrier protein synthesis (EC 2.7.8.7) (Holo-ACP synthase)
DE          DE (4'-phosphopantetheinyl transferase acps).
OS          ACPS OR IL0843.
OS          Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC          Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX          NCBI_TaxId=11601;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN=IL1403;
RC          MEDLINE=21235186; PubMed=11337471;
RA          Bojoltin A., Wincker P., Manger S., Jallion O., Malarme K.,
RA          Weissenbach J., Ehrlich S.D., Sorokin A.;
RT          "The complete genome sequence of the lactic acid bacterium Lactococcus
RL          lactis ssp. lactis IL1403."
CC          Genome Res. 11:731-753(2001).
CC          -1 FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC          A to a set of acyl-carrier protein (By similarity).
CC          -1 CATALYTIC ACTIVITY: CoA + apo-lacyl-carrier protein] = adenosine
CC          3',5'-bisphosphate + holo-[lacyl-carrier protein].
CC          -1 COPROCTOR: Magnesium (by similarity).
CC          -1 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC          -1 SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC          FAMILY.
Cc          -----
Cc          This SWISS-PROT entry is copyright. It is produced through a collaboration
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Cc          or send an email to licenses@isb-sib.ch).
Cc          -----
Cc          DR EMBL; AE006318; AAC04941.1; -.
Cc          DR PIR; C86730; C86730.
Cc          DR HAMAP; MF_00101; -: 1.
Cc          DR InterPro; IPR002582; ACPS.
Cc          DR InterPro; IPR004568; Pantethn_tm.
Cc          DR Pfam; PF01646; ACPS; 1.
Cc          DR ProDom; PD004282; ACPS; 1.
Cc          DR TIGRFAMS; TIGR00516; acps; 1.
Cc          DR TIGRFAMS; TIGR00556; pantethn_tm; 1.
Cc          KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
Cc          Complete proteome.
Cc          FT METAL             8
Cc          FT METAL             8 MAGNESIUM (BY SIMILARITY).
Cc          ST          59          MAGNESIUM (BY SIMILARITY).
Cc          SQ SEQUENCE   119 AA; 13309 MW; 1F57300FB466A9 CRC64;

Query Match           48.9%; Score 302; DB 1; Length 119;
Best Local Similarity 51.3%; Pred. No. 2,le-25;
Matches    61; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

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RESULT 7
ACPS_BACHD STANDARD; PRT; 119 AA.
ID ACPS_BACHD
AC Q9RFG1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR BH0518.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RA MEDLINE=20512582; Pubmed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AP001508; BAB04237.1; -.
DR PIR; P83714; F83714.
DR HAMAP; MF 00101; -.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_tm.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn_tm; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13421 MW; 227955254904109 CRC64;

Query Match 45.1%; Score 279; DB 1; Length 119;
Best Local Similarity 52.6%; Pred. No. 4, 2e-21;
Matches 61; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

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DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR OB0619.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxId=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RA MEDLINE=22220767; Pubmed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AP004595; BAC12575.1; -.
DR HAMAP; MF 00101; -.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn_tm; 1.
KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KW Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13474 MW; 2A6757EEA5A574DE CRC64;

Query Match 45.1%; Score 278.5; DB 1; Length 119;
Best Local Similarity 47.4%; Pred. No. 4, 7e-21;
Matches 55; Conservative 26; Mismatches 34; Indels 1; Gaps 1;

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RESULT 8
ACPS_OCEIH STANDARD; PRT; 119 AA.
ID ACPS_OCEIH
AC Q9BSK3;

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RESULT 9
ACPS_BACSU STANDARD; PRT; 121 AA.
ID ACPS_BACSU
AC P96618;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1423;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
RT "A 148 kbp sequence of the region between 35 and 47 degree of the
RL Bacillus subtilis genome."
RN Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RP
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerth I.F., Cummings N.J., Daniel R.A.,
RA Delizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Filtz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haeche J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Katamata D., Kasahara Y., Kleier-Blanchard M., Klein C.,
RA Kobayashi Y., Koelter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellido R.P., Mizuno M., Moesti D., Nakai S., Nodack M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Pirescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche B., Roche R., Rose M., Sadie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemori A.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambur R., Wedler E., Wedler H., Weissenberger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumestein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-lacyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-lacyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC -----
DR EMBL, AB001488; BAA19299.1; -
DR EMBL, 299106; CAB12269.1; -
DR PIR, H69772; H69772.
DR PDB, 1F7L; 27-JUN-01.
DR PDB, 1F7T; 27-JUN-01.
DR PDB, 1F80; 15-MAY-02.
DR Subtilist; BG12089; acps.
DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_tm.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRPAWS; TIGR00516; acps; 1.
DR TIGRPAWS; TIGR00556; pantethn_tm; 1.

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KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KM Complete proteome; 3D-structure.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 58 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 121 AA; 13718 MW; 6C10401DA7116701 CRC64;
Query Match 40.6%; Score 251; DB 1; Length 121;
Best local similarity 44.6%; Pred. No. 2,7e-18;
Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;
QY 3 MIVHGIDIDELISAEAVTRHESFARVLTQEMEPFSLKGRQIEVYLAGRMSAKAEF 62
DB 1 MIVGIGDIDELIKRISAMAGROKRFARILTRSHLDQYELSEKRNKFLAGRAKAEAF 60
QY 63 SKAMGTGISK-LGPODEVUNNNGAAY-----FSQAPFSGKIMLSHDDQFTASYIL 116
DB 61 SKAFGIGIGRQSLSDIPIKDKNGKRYITCKLSQA-----AVHVSITHREYAAQVVI 116
QY 117 E 117
DB 117 E 117
RESULT 10
ACPS_LISMO STANDARD; PRT; 118 AA.
ID ACPS_LISMO
AC O8Y8L2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holo-lacyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR LMO0885.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxId=1639;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
RA Baguero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-lacyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-lacyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AL591977; CAC98963.1; -
DR PIR, AE1185; AE1185.
DR Listlist; LMO00885; -.

```

DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Panlethn_tm.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; panlethn_tm; 1.
 DR Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KM Complete proteome.
 FT METAL 8
 FT METAL 8 MAGNESIUM (BY SIMILARITY).
 FT METAL 58 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 118 AA; 13257 MW; 5584C5C769181B3F CRC64;

Query Match 37.7%; Score 233; DB 1; Length 118;
 Best Local Similarity 42.7%; Pred. No. 1.6e-16;
 Matches 50; Conservative 30; Mismatches 35; Indels 2; Gaps 2;

QY 3 MIVGHGIDIELASIESAVTRHEGFARVLTAEEMERFTSLKGRQTEYLGRWSAKEAF 62
 Db 1 MIVGIGLMDLDRVKQAVEKNPRFIERLTETKTKQYKESGRKTEFLAGRAAKAY 60

QY 63 SKAMGTGISK-LGPQDEVVNNEGARYFSQAPPSGK-INDSHTQFVTASYILE 117
 Db 61 AKANGTGFHSLFTDVEILLQVEDGRPHVTLPVKSGENVVSIHTARSAAYIIE 117

RESULT 11
 ACPS_LISIN STANDARD; PRT; 118 AA.
 ID Q92DD0;
 AC 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS OR LIN0884.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

NCBI_TaxID=1642;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaeser P., Frangoul L., Buchrieser C., Rusanick C., Amend A.,
 BA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
 RA Charbit A., Cherouani F., Couve E., de Daruvar A., Deloux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fish H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kurupkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz U.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tixeret A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RL "Comparative genomics of *Listeria species.*";
 Science 294:849-852 (2001).

CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
 FAMILY.

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DR EMBL; AL596166; CAC96116.1; -.
 DR PIR; AD1543; AD1543.
 DR Listlist; LIN00884; -.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Panlethn_tm.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; panlethn_tm; 1.
 DR Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KM Complete proteome.
 FT METAL 8
 FT METAL 58 MAGNESIUM (BY SIMILARITY).
 FT METAL 58 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 118 AA; 13281 MW; BFC89CFF84BCB985 CRC64;

Query Match 36.9%; Score 228; DB 1; Length 118;
 Best Local Similarity 40.7%; Pred. No. 5.2e-16;
 Matches 48; Conservative 32; Mismatches 36; Indels 2; Gaps 2;

QY 3 MIVGHGIDIELASIESAVTRHEGFARVLTAEEMERFTSLKGRQTEYLGRWSAKEAF 62
 Db 1 MIVGIGLMDLDRVKQAVEKNPRFIERLTETKTKQYKESGRKTEFLAGRAAKAY 60

QY 63 SKAMGTGISK-LGPQDEVVNNEGARYFSQAPPSGK-INDSHTQFVTASYILE 118
 Db 61 AKANGTGFHSLFTDVEILLQVEDGRPHVTLPVKSGENVVSIHTARSAAYIIE 118

RESULT 12
 ACPS_LACRE STANDARD; PRT; 117 AA.
 ID Q9FCV3;
 AC 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS.
 OS Lactobacillus reuteri.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.

NCBI_TaxID=1598;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 53608;
 RA Thompson A., Griffin H., Gasson M.J.;
 RT "Cloning and characterisation of an alanine racemase gene from
 RT Lactobacillus reuteri";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- CORFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
 FAMILY.

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DR EMBL; AJ278312; CAC03496.1; ALT_INT.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Panlethn_tm.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.

DR TIGRFAMS; TIGR00516; acps, 1.
 DR TIGRFAMS; TIGR00556; pantethn_tm, 1.
 KW Transferrase; Lipid synthesis; Fatty acid biosynthesis; Magnesium.
 FT METAL 8 MAGNESIUM (BY SIMILARITY).
 FT METAL 57 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 117 AA; 12944 MW; 2A7D5807064325C8 CRC64;

Query Match 35.8%; Score 221; DB 1; Length 117;
 Best Local Similarity 44.0%; Pred. No. 2.6e-15;
 Matches 51; Conservative 17; Mismatches 46; Indels 2; Gaps 2;

Qy 3 MIVHGDIIEELASIESAVTHRGFAKAVLTAQEMERTSI-KRRQIEYLAGRWSAKEAF 62
 Db 1 MIVGIDITIDIRK-ALHNPTSIKKVLTDRQALAGKSGQRAVEFFLAGHFSVKESEY 59
 63 SKAMGTGI-SKLGFDLELVNNGAPYFSGAPFSGKIMLSHSDQFVTA5VILE 117
 Db 60 SKAIGTGKGLKNQDIEVEYDDNGRPVTSNHPAGVAHVSISSKHVTVQVILE 115

RESULT 13

ACPS_STAUV STANDARD; PRT; 119 AA.
 AC 09ZAH6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 GN ACPS OR DBJ
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 8325;
 RX MBLINE=98434453; PubMed=9756984;
 RA Kullik I., Jenni R., Berger-Becchi B.;
 RT "Sequence of the putative alanine racemase operon in Staphylococcus aureus: insertional interruption of this operon reduces D-alanine substitution of lipoteichoic acid and autolysis."
 RL Gene 219:9-17(1998).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (By similarity).
 CC CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS FAMILY.

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CC EMBL; Y16431; CA76220.1; -
 DR HAMAP; MF 00101; -; 1.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantethn_tm.
 DR Pfam; PF01648; ACPS; 1.
 DR Pfam; PD004282; ACPS; 1.
 DR TIGRFAMS; TIGR00516; acps, 1.
 DR TIGRFAMS; TIGR00556; pantethn_tm, 1.
 KW Transferrase; Lipid synthesis; Fatty acid biosynthesis; Magnesium.
 FT METAL 8 MAGNESIUM (BY SIMILARITY).
 FT METAL 59 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 119 AA; 13605 MW; 0B82BA811774B188 CRC64;

Query Match 34.3%; Score 212; DB 1; Length 119;

Best Local Similarity 37.8%; Pred. No. 2.1e-14;
 Matches 45; Conservative 30; Mismatches 40; Indels 4; Gaps 3;

Qy 3 MIVHGDIIEELASIESAVTHRGFAKAVLTAQEMERTSI-KRRQIEYLAGRWSAKEA 61
 Db 1 MIVHGDIIEELASIESAVTHRGFAKAVLTAQEMERTSI-KRRQIEYLAGRWSAKEA 60

Qy 62 FSKAMGTGSK-LGFQDLELVNNGAPYFSGAPFSGKIMLSHSDQFVTA5VILE 119
 Db 61 FSKALGTGKGLKNQDIEVEYDDNGRPVTSNHPAGVAHVSISSKHVTVQVILE 117

RESULT 14

ACPS_VIBVU STANDARD; PRT; 126 AA.
 AC 08C72;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 GN ACPS OR V11569.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMC6;
 RA Rhee U.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of Vibrio vulnificus CMC6."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (By similarity).
 CC CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS FAMILY.

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CC EMBL; AE016802; AAC09993.1; -
 DR HAMAP; MF 00101; -; 1.
 DR Pfam; PF01648; ACPS; 1.
 DR Pfam; PD004282; ACPS; 1.
 DR TIGRFAMS; TIGR00516; acps, 1.
 DR TIGRFAMS; TIGR00556; pantethn_tm, 1.
 KW Transferrase; Lipid synthesis; Fatty acid biosynthesis; Magnesium.
 FT METAL 9 MAGNESIUM (BY SIMILARITY).
 FT METAL 58 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 126 AA; 13633 MW; 80BDE9222F04E78E CRC64;

Query Match 34.1%; Score 210.5; DB 1; Length 126;
 Best Local Similarity 42.4%; Pred. No. 3.1e-14;
 Matches 53; Conservative 22; Mismatches 37; Indels 13; Gaps 4;

Qy 4 IIVHGDIIEELASIESAVTHRGFAKAVLTAQEMERTSI-KRRQIEYLAGRWSAKEAF 62
 Db 3 IIVHGDIIEELASIESAVTHRGFAKAVLTAQEMERTSI-KRRQIEYLAGRWSAKEAF 60
 63 SKAMGTGSK-LGFQDLELVNNGAPYFSGAPFSGKIMLSHSDQFVTA 112
 Db 61 SKALGTGKGLKNQDIEVEYDDNGRPVTSNHPAGVAHVSISSKHVTVQVILE 120

Qy 113 SVILE 117
 Db 121 TWIFE 125

RESULT 15
 ACPS STAM

ID ACPS STAM STANDARD; PRT; 119 AA.

AC Q99S14;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Holo-lacyl-carrier protein synthase (EC 2.7.8.7) (Holo-ACP synthase)

(4'-phosphopantetheinyl transferase acps)

GN ACPS OR DBU OR SAY2071 OR SA1875 OR MW1995.

OS Staphylococcus aureus (strain M50 / ATCC 700699),

OS Staphylococcus aureus (strain N315), and

OS Staphylococcus aureus (strain MW2).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=158878, 158879, 196620;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=M50 / ATCC 700699, and N315;

RX MEDLINE=21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RT "Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus."

RL Lancet 357:1225-1240 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=MW2;

RX MEDLINE=22040717; PubMed=12044378;

RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,

RA Nagai Y., Iwama N., Asano K., Naiml T., Kuroda H., Cui L.,

RA Yamamoto K., Hiramatsu K.;

RT "Genome and virulence determinants of high virulence community-

RT acquired MRSA."

RL Lancet 359:1819-1827 (2002).

CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme

CC A to a Ser of acyl-carrier protein (By similarity).

CC -!- CATALYTIC ACTIVITY: CoA + apo-lacyl-carrier protein] = adenosine

CC 3',5'-bisphosphate + holo-lacyl-carrier protein).

CC -!- COFACTOR: Magnesium (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS

CC FAMILY.

CC -----

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CC -----

CC EMBL, AP003364; BAB58233.1; -

CC EMBL, AP003136; BAB43158.1; -

CC EMBL, AP004829; BAB95860.1; -

CC FTR, E89999; E89999.

CC HAMAP, MF_00101; -; 1.

CC InterPro; IPR002582; ACPS.

CC InterPro; IPR004568; Pantethn_tm.

CC Pfam; PF01648; ACPS; 1.

CC ProDom; PD004282; ACPS; 1.

CC TIGRfams; TIGR00516; acps; 1.

CC TIGRfams; TIGR00556; pantethn_tm; 1.

KW Transferase; lipid synthesis; Fatty acid biosynthesis; Magnesium;
 KM Complete proteome.
 FT METAL 8
 FT METAL 59
 SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match

Best Local Similarity 33.7%; Score 208; DB 1; Length 119;

Matches 45; Conservative 29; Mismatches 41; Indels 4; Gaps 3;

Qy 3 MIVGHGIDIELASIESAVTRHGFAPKRVLTAEOMERFSL-KGRROIYLAGMSAKEA 61

Db 1 MIVGHGIDIELRIKIVLSKQPKVLRILTKQEHKFNFTHEORKIEFLAGRPATVEA 60

Qy 62 PSKAMGTGISK-LGFODLEVLNNEGAPYPSQAPFSGKIVLSISHTDQFVTAIVLEEN 119

Db 61 FSKALGTGIGKVAHFNDICYNDELGKPKIDYEGFI--VHVSISHTHYAMSQVLEKS 117

Search completed: December 10, 2003, 19:35:35
 Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 19:32:36 ; Search time 35 Seconds
(without alignments)
899.498 Million cell updates/sec

Title: US-09-897-645-1
Perfect score: 618
Sequence: 1 MNMIVGHGIDIEELASIESA.....ISHTDPVTASVILEENHS 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvivirus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	64.2	119	16 Q8DSF3	Q8df3 streptococ
2	328.5	53.2	119	16 Q8E3M8	Q8e3m8 streptococ
3	328.5	53.2	119	16 Q8DY09	Q8dy09 streptococ
4	278.5	45.1	119	16 Q8E3K9	Q8e3k9 oceanobacil
5	212.5	34.4	74	2 O07122	O07122 lactobacill
6	210.5	34.1	126	16 Q8DC72	Q8dc72 vibrio vuln
7	199.5	32.3	117	16 Q8CNK6	Q8cnk6 staphylococ
8	176	28.5	139	16 Q8D303	Q8d303 wiggleswort
9	176	28.5	158	5 Q8MNP2	Q8mnp2 dictyostell
10	150.5	24.4	127	16 Q8EH77	Q8eh77 shewanella
11	148.5	24.0	126	16 Q8FF19	Q8ff19 escherichia
12	127	20.6	1858	3 P78615	P78615 emeticella
13	114.5	18.5	126	16 Q8F136	Q8f136 leptospira
14	108	17.5	153	2 O31302	O31302 corynebacte
15	107	17.3	377	3 P78866	P78866 schizosacch
16	107	17.3	1842	3 Q96WT6	Q96wt6 schizosacch

17	107	17.3	1842	3 Q96WT7	Q96wt7 schizosacch
18	107	17.3	1842	3 Q96WT8	Q96wt8 schizosacch
19	106.5	17.2	120	16 Q8EX15	Q8ex15 mycoplasma
20	101	16.3	275	2 Q93M10	Q93m10 streptomyce
21	96	15.5	314	4 Q9C068	Q9c068 homo sapien
22	95.5	15.5	230	16 Q8DTK3	Q8dtk3 streptococ
23	91.5	14.8	141	16 Q8FMO0	Q8fmo0 corynebacte
24	89	14.4	244	16 Q8F8B0	Q8f8b0 escherichia
25	89	14.4	481	6 Q97641	Q97641 equus cabal
26	88	14.2	181	16 Q8G455	Q8g455 bifidobacte
27	85	13.8	211	4 Q9UG80	Q9ug80 homo sapien
28	85	13.8	309	4 Q9Y389	Q9y389 homo sapien
29	85	13.8	309	4 Q9P0Q3	Q9p0q3 homo sapien
30	85	13.8	333	4 Q9NRN7	Q9nrn7 homo sapien
31	84	13.6	594	5 Q8I1N7	Q8i1n7 plasmodium
32	83	13.4	242	2 Q9ZAZ7	Q9zaz7 streptomyce
33	82.5	13.3	280	2 Q931X7	Q931x7 streptomyce
34	82	13.3	177	3 Q12036	Q12036 saccharomyce
35	81	13.1	264	2 Q93H53	Q93h53 streptomyce
36	81	13.1	1523	2 Q93H10	Q93h10 streptomyce
37	79.5	12.9	1671	3 Q8TGA2	Q8tga2 aspergillus
38	79	12.8	210	11 Q9CU40	Q9cu40 mus musculu
39	79	12.8	309	11 Q9COF6	Q9cof6 mus musculu
40	78.5	12.7	207	16 Q8CTM4	Q8ctm4 staphylococ
41	78.5	12.7	300	10 Q8YTK1	Q8ytk1 arabidopsis
42	78.5	12.7	2044	16 Q8Y8Q4	Q8y8q4 listeria mo
43	77.5	12.5	217	10 Q98722	Q98722 artocarpus
44	77.5	12.5	261	16 Q9KAL7	Q9kal7 bacillus ha
45	76.5	12.4	217	10 Q98720	Q98720 artocarpus

ALIGNMENTS

RESULT 1	Q8DSF3	PRELIMINARY;	PRT;	119 AA.
AC	Q8DSF3;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Putative acyl carrier protein synthase, AcpS (EC 2.7.8.7).			
GN	ACPS OR SMU.1835.			
OS	Streptococcus mutans.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1309;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=UAI59 / ATCC 700610 / Serotype C;			
RX	MEDLINE=22295063; PubMed=12397186;			
RA	Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,			
RA	Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin Y.,			
RA	Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;			
RT	Genome sequence of Streptococcus mutans UAI59, a cariogenic dental			
RT	pathogen."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).			
DR	EMBL; AB015010; AAN59458.1; -			
KW	Transferase; Complete proteome.			
SQ	SEQUENCE 119 AA; 13218 MW; 450139C210FEF866 CRC64;			

QY	Query Match	64.2%;	Score 397;	DB 16;	Length 119;
DB	Best Local Similarity	62.7%;	Pred. No. 2.8e-33;		
	Matches 74;	Conservative 24;	Mismatches 20;	Indels 0;	Gaps 0;
QY	3 MNMIVGHGIDIEELASIASATVTRHGKRVLTQEMERFSLKGRQIEYLAGWSAKAF 62				
DB	1 MNMIVGHGIDIEELASIASATVTRHGKRVLTQEMERFSLKGRQIEYLAGWSAKAF 60				
QY	63 SKAMGTGSKLQGVDDVLENNRGAFFYQAPFSGKWTLSHTDQFVTASVILEENH 120				
DB	61 SKAYGSGISLRFQDEILANNKGAIFPKSPFSGNIFISHSKNYVESVILEENH 118				

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RESULT 2
Q8E3M8 PRELIMINARY; PRT; 119 AA.
AC Q8E3M8:
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical protein.
GN GBS1729.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaser P., Rasmick C., Buchrieser C., Chevalier F., Frangeul L.,
RA Masdek T., Zouine M., Couve E., Lallouf L., Poyart C., Tieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766852; CAD47388.1; -.
KW Sagalistic; gbs1729; -.
SQ SEQUENCE 119 AA; 13268 MW; COEB77DA27C5C2E CRC64;

Query Match 53.2%; Score 328.5; DB 16; Length 119;
Best Local Similarity 52.1%; Pred. No. 3.3e-26;
Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 3 MIVGHGIDIEBLASIESAVTRHSGFAKRVLTQAQMERFTSLKG-RROIEYLGRWSAKEA 61
D 1 MIVGHGIDIEBLASIESAVTRHSGFAKRVLTQAQMERFTSLKG-RROIEYLGRWSAKEA 60
D 62 FSKMGVGTISKLGFQDLEVLNNGRGAAPFSGAPSGKIMLSHTDQFVTASVILEE 118
D 61 YSKALGTGIGKVNPHDIEILSDDKGAPLITKEPFGKSFVSIHSGNVAQASVILEE 117

Db
QY 62 FSKMGVGTISKLGFQDLEVLNNGRGAAPFSGAPSGKIMLSHTDQFVTASVILEE 118
D 61 YSKALGTGIGKVNPHDIEILSDDKGAPLITKEPFGKSFVSIHSGNVAQASVILEE 117

RESULT 3
Q8DYO9 PRELIMINARY; PRT; 119 AA.
AC Q8DYO9:
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Holo-(acyl-carrier-protein) synthase.
GN ACS OR SAG1685.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547;
RA Tetteijn H., Masigiani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelsen K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scanlan D., Knouti H., Mulligan S.,
RA Carthy H.A., Cline R.T., Van Aken S.E., Gill J., Scarelli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AB014268; AA000549.1; -.
TI GR; SAG1685; -.

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KW Complete proteome.
SQ SEQUENCE 119 AA; 13268 MW; COEB77DA27C5C2E CRC64;

Query Match 53.2%; Score 328.5; DB 16; Length 119;
Best Local Similarity 52.1%; Pred. No. 3.3e-26;
Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 3 MIVGHGIDIEBLASIESAVTRHSGFAKRVLTQAQMERFTSLKG-RROIEYLGRWSAKEA 61
D 1 MIVGHGIDIEBLASIESAVTRHSGFAKRVLTQAQMERFTSLKG-RROIEYLGRWSAKEA 60
D 62 FSKMGVGTISKLGFQDLEVLNNGRGAAPFSGAPSGKIMLSHTDQFVTASVILEE 118
D 61 YSKALGTGIGKVNPHDIEILSDDKGAPLITKEPFGKSFVSIHSGNVAQASVILEE 117

Db
QY 62 FSKMGVGTISKLGFQDLEVLNNGRGAAPFSGAPSGKIMLSHTDQFVTASVILEE 118
D 61 YSKALGTGIGKVNPHDIEILSDDKGAPLITKEPFGKSFVSIHSGNVAQASVILEE 117

RESULT 4
Q8E3K9 PRELIMINARY; PRT; 119 AA.
AC Q8E3K9:
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Holo-(acyl carrier protein) synthase.
GN OB0619.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AP004595; BAC12575.1; -.
KW Complete proteome.
SQ SEQUENCE 119 AA; 13474 MW; 2AF757EEAE574DE CRC64;

Query Match 45.1%; Score 278.5; DB 16; Length 119;
Best Local Similarity 47.4%; Pred. No. 4.8e-21;
Matches 55; Conservative 26; Mismatches 34; Indels 1; Gaps 1;

QY 3 MIVGHGIDIEBLASIESAVTRHSGFAKRVLTQAQMERFTSLKG-RROIEYLGRWSAKAF 62
D 1 MIVGHGIDIEBLASIESAVTRHSGFAKRVLTQAQMERFTSLKG-RROIEYLGRWSAKAF 60
D 63 SKMGVGTISKLGFQDLEVLNNGRGAAPFSGK-IMLSHTDQFVTASVILEE 117
D 61 AKAVGTGIGKVSFDDIEILNNDYGAPPMKVGNDVNIHLSHSHSKTYAVANVILEE 116

Db
QY 63 SKMGVGTISKLGFQDLEVLNNGRGAAPFSGK-IMLSHTDQFVTASVILEE 117
D 61 AKAVGTGIGKVSFDDIEILNNDYGAPPMKVGNDVNIHLSHSHSKTYAVANVILEE 116

RESULT 5
Q07122 PRELIMINARY; PRT; 74 AA.
AC Q07122:
DT 01-JUN-1997 (TREMblrel. 04, Created)
DT 01-JUN-1997 (TREMblrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical 8.0 kDa protein (Fragment).
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIM8826;
RX MEDLINE=9731526; PubMed=9171436;
RA Hols P., Defreene C., Ferain T., Derzelle S., Delcour J.;
RT "The alanine racemase gene is essential for growth of Lactobacillus
RT plantarum."

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RL J. Bacteriol. 179:3804-3807(1997).
 DR EMBL: Y08941; CAA70142.1; -.
 DR HSSP: Q9F7T5; 1FTH.
 DR InterPro: IPR002582; ACPS.
 DR InterPro: IPR004568; Panlethn_tm.
 DR Pfam: PF01648; ACPS; 1.
 DR ProDom: PD004282; ACPS; 1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 74 AA; 8039 MW; 32137591876D001A CRC64;

Query Match 34.4%; Score 212.5; DB 2; Length 74;
 Best Local Similarity 56.2%; Pred. No. 1.7e-14;
 Matches 41; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 49 IEVLAGWSAKFAKSKAMGTG-SKLGFDLEVLNNGRGAPYFSQAPFSKIMLSHTD 107
 DB 1 IEFMAGFFSAKFAKSKAYGTGIGAVGFQDIEILDNAQKPEVTRHFDGPAWLSISHTD 60
 QY 108 QFYTASYILEEN 120
 DB 61 TLVMTQVILERN 73

RESULT 6
 ID Q8DC72 PRELIMINARY; PRT; 126 AA.
 AC Q8DC72;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phosphopantetheinyl transferase.
 GN W11569.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OC NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB016802; AAC09993.1; -.
 KW transferase; Complete proteome.
 SQ SEQUENCE 126 AA; 13633 MW; 80BDE9222F04E78E CRC64;

Query Match 34.1%; Score 210.5; DB 16; Length 126;
 Best Local Similarity 42.4%; Pred. No. 5.4e-14;
 Matches 53; Conservative 22; Mismatches 37; Indels 13; Gaps 4;

QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEMERFTSLKGRQIEVLAGWSAKFA 62
 DB 3 IVGLGDIADIEIRERKALARSQVAFARILISAQEMETFVSLK--QGRFLAKKFAKFA 60
 QY 63 SKAMGIGISK-LGFQDLEVLNNGRGAPYFSQAPFSKIMLSHTDQFVTA 112
 DB 61 SKALGTGIAHGVSFQDFTTKNDNGKPYQLAGRAAELAHQMGVCHTHLSIDRHYAVA 120

QY 113 SVILE 117
 DB 121 TVIFE 125

RESULT 7
 ID Q8CNK6 PRELIMINARY; PRT; 117 AA.
 AC Q8CNK6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Holo-ACP synthase.

GN SE1675
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB016749; AAC05274.1; -.
 KW Complete proteome.
 SQ SEQUENCE 117 AA; 13535 MW; 515246BC14DEDC9 CRC64;

Query Match 32.3%; Score 199.5; DB 16; Length 117;
 Best Local Similarity 38.7%; Pred. No. 6.7e-13;
 Matches 46; Conservative 27; Mismatches 41; Indels 5; Gaps 4;

QY 3 MIVGHGIDIEELASIESAVTRHESFAKRVLTQAEMERFTSLKGRQIEVLAGWSAKFA 61
 DB 1 MIVGIGIDIEIRIKR-LQNGTKFYERILIERDRDLNQTHTORLEFLAGRFYVAA 59
 QY 62 FSKAMGTGISK-LGFQDLEVLNNGRGAPYFSQAPFSKIMLSHTDQFVTA 119
 DB 60 FSKALGTGIGKSVSFQDINCYNDAIGKPCIDYEGFYTHV--SITHLENYAMQVILEKN 116

RESULT 8
 ID Q8D303 PRELIMINARY; PRT; 139 AA.
 AC Q8D303;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ACPs protein.
 GN ACPS.
 OS Wigglesworthia brevipalpis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Wigglesworthia.
 OC NCBI_TaxID=164609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=2297718; PubMed=12219091;
 RA Akman L., Yamashita A., Watanabe H., Oshina K., Shida T., Hattori M.,
 RA Aksoy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT flies, *Wigglesworthia glossinidia*."
 RL Nat. Genet. 32:402-407(2002).
 DR EMBL: AB063521; BAC24344.1; -.
 KW Complete proteome.
 SQ SEQUENCE 139 AA; 15871 MW; CD9084121DCF8897 CRC64;

Query Match 28.5%; Score 176; DB 16; Length 139;
 Best Local Similarity 36.2%; Pred. No. 2.2e-10;
 Matches 47; Conservative 23; Mismatches 46; Indels 14; Gaps 4;

QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEMERFTSLKGRQ--IEVLAGWSAK 59
 DB 3 IIGIGIDIVLIERINKITILCYGNKFVKILISFEKKKKYELKKKKKISVFLAKRLAK 62
 QY 60 EAFSKAMGTGISK-LGFQDLEVLNNGRGAPYFS-----QAPFSKIMLSHTDQF 109
 DB 63 EAASKAFGLGMKKGLYFSQFEVLNNNLGKPYFKNNTAKULIRALITNTIHLSTDERKY 122

QY 110 VTSVILEEN 119
 DB 123 ACATVIFEDN 132

RESULT 9
 ID Q8MNP2 PRELIMINARY; PRT; 158 AA.
 AC Q8MNP2;
 DT 08MNP2;
 DT 08MNP2;


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DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gleicher G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tünggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116961; AAM33765.1; -.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Panteln_tm.
DR Prodom; PD004282; ACPS.1.
DR TIGRFAMs; TIGR00516; acps.1.
DR TIGRFAMs; TIGR00556; panteln_tm.1.
KM Hypothetical protein.
SQ SEQUENCE 158 AA; 17931 MW; AAE56FBF387B08EB CRC64;

Query Match 28.5%; Score 176; DB 5; Length 158;
Best Local Similarity 30.7%; Pred. No. 2.6e-10;
Matches 50; Conservative 21; Mismatches 44; Indels 48; Gaps 5;

QY 1 MRMIVGHGIDIEELASISAVTRHREGFAKRVLTQAQEMERFTSL----- 43
DB 1 MNKIFGIGNDIVKISRLSSSF-----KRAFNEVEISIFSLNPTASITSIDNDNSE 53

QY 44 -----KRRQIYILAGRWSAKEAFSKAMGT-GISKIGFQDLEVLNNGCAP 88
DB 54 LANNNNNNNNNNNNNNNGFEYLAGRWAKESIKYALINQDRSKLNFQNIQLNESMRP 113

QY 89 YF-----SQAPFS-----GKIWLISHTQGFVTAFTLEENHES 122
DB 114 YVNILETTESYFKELGINKILALSHEDVLAISNVILESNST 156

RESULT 10
Q8EH77 PRELIMINARY; PRT; 127 AA.
ID Q8EH77
AC Q8EH77
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Holo-(acyl-carrier protein) synthase.
GN ACPS OR S01352.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RA Heidelberg J.F., Paulsen I.T., Neilson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Meche B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Ullrich J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015579; AAN54417.1; -.
DR TIGR; S01352; -.
KM Complete proteome.
SQ SEQUENCE 127 AA; 13638 MW; 6CA5CC686C50F2A0 CRC64;

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Query Match 24.4%; Score 150.5; DB 16; Length 127;
Best Local Similarity 37.6%; Pred. No. 8.4e-08;
Matches 47; Conservative 22; Mismatches 43; Indels 13; Gaps 6;

QY 4 IVGHGIDIEELASISAVTRH-EGFAKRVLTQAQEMERFTSLKGRQIEYLGRWSAKAF 62
DB 3 IVGLGTDIVETRIEISAVHARGDLARVLTAEAFETIQ--QHSQPSRYLKKRPAAKAA 60

QY 63 SKAMGTGISK-IGFQDLEVLNNGCAPY--FSCAP-----FSGKI-WLSISHTQGFVTA 112
DB 61 AKALGTGIGRVSQHHIGNTPGCAPITDTEBAQQRLLTNNGVGHISIADESVYIA 120

QY 113 SVILE 117
DB 121 TVILE 125

RESULT 11
Q8FF19 PRELIMINARY; PRT; 126 AA.
ID Q8FF19
AC Q8FF19
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Holo-(acyl-carrier protein) synthase (EC 2.7.8.7).
GN ACPS OR C3087.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / ATCC 700928;
RA MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosch P.,
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016764; AAN81536.1; -.
KM Transferase; Complete proteome.
SQ SEQUENCE 126 AA; 14152 MW; 4D0738210F742AFF CRC64;

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Query Match 24.0%; Score 148.5; DB 16; Length 126;
Best Local Similarity 31.8%; Pred. No. 1.3e-07;
Matches 42; Conservative 25; Mismatches 38; Indels 27; Gaps 5;

QY 4 IVGHGIDIEELASISAVTRH-EGFAKRVLTQAQEMERFTSLKGRQIEYLGRWSAKAF 62
DB 3 ILGLGTDIVETRIEISAVHARGDLARVLTAEAFETIQ--HHQPVAFKKRFVAKAA 60

QY 63 SKAMGTGISK-IGFQDLEVLNNGCAPYFSCAPSSGKIT-----LSISH 105
DB 61 AKAFGTGIRGLANQREVEFDELGKPRL-----RLWGBALKLAEXLGVVNMHTVLAD 113

QY 106 TDQGFVTA 117
DB 114 ERHVAACKTVILE 125

RESULT 12
P78615 PRELIMINARY; PRT; 1858 AA.
ID P78615
AC P78615
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Fatty acid synthase, alpha subunit.
GN FASA.
OS Emricella nidulans (Aspergillus nidulans).

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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121482; PubMed=8962148;
RA Brown D.W., Adams T.H., Keller N.P.;
RT "Aspergillus has distinct fatty acid synthases for primary and
RT secondary metabolism."
RL EMBL; U75347; AAB41493.1; -.
DR HSSP; Q9P7T5; 1PTF.
DR InterPro; IPR002582; ACPs.
DR InterPro; IPR000794; Ketoacyl-synt.
DR InterPro; IPR004568; Pantethn_trn.
DR InterPro; IPR006162; Pantane_attach.
DR Pfam; PF01648; ACPs; 1.
DR Pfam; PF0109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR Prodom; PD004282; ACPs; 1.
DR TIGRfam; TIGR00556; pantethn_trn; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
DR TRANSFERASE.
SQ SEQUENCE 1858 AA; 204730 MW; 3D961E8716C9E24D CRC64;

Query Match 20.6%; Score 127; DB 3; Length 1858;
Best Local Similarity 34.2%; Pred. No. 0.00071;
Matches 40; Conservative 18; Mismatches 45; Indels 14; Gaps 5;

QY 8 GIDIEELASIESAVTRHEGFAKRVLTQEMERFSLKGRQIEYLGRMSAKAFSGKMG 67
Db 1744 GVDV---SIDSNINISNETIERILPSEDOYCONAPSPD--SSPGRMSAKAFVPSLIG 1798
QY 68 TGISKLQ--FQDLEVLNNERGAFF-----SQAPFSG--KIMLSISHTDQFTASVIL 115
Db 1799 VCSKGAAPLKQIEIENDSGCAPTLHGVAABAKEAGVKRISVISHSDMGAVAVAI 1855

RESULT 13
Q8F136 PRELIMINARY; PRT; 126 AA.
ID Q8F136
AC Q8F136;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Phosphopantetheinyl transferase (EC 2.7.8.7).
OS ACPs OR IA3302.
OS Leptosira interogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptosira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A6011490; AAN50500.1; -.
DR TRANSFERASE; Complete proteome.
SQ SEQUENCE 126 AA; 14419 MW; F7C32E3F9C289785 CRC64;

Query Match 18.5%; Score 114.5; DB 16; Length 126;
Best Local Similarity 32.0%; Pred. No. 0.00043;
Matches 41; Conservative 23; Mismatches 47; Indels 17; Gaps 6;

QY 1 MNMIVGHGIDIEELASIESAVTRH-BGFAKRVLTQEMERFSLKGRQIEYLGRWSAK 59
Db 1 MKISVGN--DIVNSHRIIDLKRGDRFLKRVFSESESEYCSNRKD--PIPHLSGRFCVK 56
QY 60 EAFSKMGTGISK-LGFQDLEVLNNERG-----APYEQAPFSGKIMLSISHTDQ 108
Db 57 EAFKTAIEPDVILMRRIELFGKPKGKKEIVLHGSKRELFLTKGYSG--CYSVISHAEN 115
QY 109 FTASVIL 116

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Db 116 YSTAVVVL 123

RESULT 14
Q031302 PRELIMINARY; PRT; 153 AA.
ID Q031302
AC Q031302;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Phosphopantetheine protein transferase, Pftip.
OS Corynebacterium ammoniagenes (Brevibacterium ammoniagenes).
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1697;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6871;
RX MEDLINE=98004292; PubMed=9346306;
RA Stubble H.P., Meier S., Schweizer E.;
RT "Identification, isolation and biochemical characterization of a
RT phosphopantetheine:protein transferase that activates the two type-1
RT fatty synthases of Brevibacterium ammoniagenes."
RL Eur. J. Biochem. 248:481-487(1997).
DR EMBL; Y15081; CA475358.1; -.
DR HSSP; Q9P7T5; 1PTF.
DR InterPro; IPR004568; Pantethn_trn.
DR Pfam; PF01648; ACPs; 1.
DR TIGRfam; TIGR00556; pantethn_trn; 1.
DR TRANSFERASE.
SQ SEQUENCE 153 AA; 16885 MW; ADE208DDE34EE00 CRC64;

Query Match 17.5%; Score 108; DB 2; Length 153;
Best Local Similarity 26.4%; Pred. No. 0.0026;
Matches 37; Conservative 21; Mismatches 50; Indels 32; Gaps 4;

QY 8 GIDIEELASIESAVTRHEGFAKRVLTQEMERF-----TSIKGRQIEYLGR 55
Db 11 GVDLVHIGFAEDLSRPGSTFBEQVPSLEHRHQTNRDAADATNSLAASR-TEHLAGR 69
QY 56 WSAKEAFSKMGITG-----SKLGFQDLEVLNNERG-----APYFSGAPFS 96
Db 70 WAAKEAFIRKMSQAIVGKPPVIEPDLVNFALIEVLPDRGWRVALQLKGEVAAKIQESIGD 129
QY 97 GKIMLSISHTDQFTASVIL 116
Db 130 VELALISHDGYATVACLL 149

RESULT 15
P78866 PRELIMINARY; PRT; 377 AA.
ID P78866
AC P78866;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Unknown protein (Fragment).
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetales;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshioke S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNA Res. 4:363-369(1997).
RL EMBL; D89216; BAA13877.1; -.

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DR HSSP; Q9F7T5; 1TFE.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR00794; Ketoacyl-synt.
 DR InterPro; IPR004568; Panteln_tm.
 DR Pfam; PF01648; ACPS; 1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00556; panteln_tm; 1.
 FT NON_TER 1
 SQ SEQUENCE 377 AA; 40534 MW; 2E7A8AF1B8016209 CRC64;

Query Match 17.3%; Score 107; DB 3; Length 377;
 Best Local Similarity 32.7%; Pred. No. 0.011;
 Matches 37; Conservative 19; Mismatches 37; Indels 20; Gaps 6;

QY 8 GIDIEELASIESAVTRHGFARVLTAEEMERFTSLKGRQIEYLAGRWSAKAFAFSKMG 67
 Db 261 GVDVELVSAIS--IDNETFIERNFT--DTERKYCFAPNPQASFGRWSAKAFAVFKSL- 314
 QY 68 TGISKLG---FQDLEVLNNEGAPYF-----SQAPPSG-KIMLSISHTD 107
 Db 315 -GISGKGAAAPLKDIEIISSESAGAEVVIHGSAKAAATTAGVKSVSISSHD 366

Search completed: December 10, 2003, 19:36:25
 Job time : 38 secs